

## Supporting Information Appendix

### Text S1. Methods for DNA analysis of fecal samples.

**Collecting and processing samples.** Mpala Research Centre and Conservancy is situated in semi-arid Laikipia, Kenya. Rainfall averages  $\sim$ 600 mm yr $^{-1}$  in a weakly tri-modal annual pattern with peaks in April-May (long rains), July-August (continental rains), and November (short rains), and a dry season in December-March. Samples were collected in June-July 2013.

We grab-sampled and thoroughly mixed fresh dung in unused zipper bags, avoiding the parts of dung touching soil or vegetation. Fecal samples were stored at  $\sim$ 4°C for 1 – 4 h, mixed thoroughly, and sampled ( $\sim$ 0.2 mg) for DNA extraction with a Zymo Xpedition Soil/Fecal DNA mini kit. Prior to freezing, samples were treated with proteinase K, heated to 95°C for 15 min, and treated with RNase A, as a precaution against the transport of foot-and-mouth disease (USDA APHIS permit #122489). Lysate was frozen and transported to Princeton University for DNA extraction and analysis. Samples were processed in small batches (3 – 23; typically 15) with an extraction blank to monitor for potential cross-contamination in a laboratory designed to conduct molecular diet analyses, including separate pre- and post-PCR rooms, with separate equipment for DNA extraction, PCR (including a laminar flow hood), and post-PCR processing.

**Confirming the identity of buffalo samples.** Buffalo are the scarcest large mammalian herbivore (LMH) species in our study (1) and are active nocturnally, which required us to collect fresh buffalo dung in the morning without observing defecation. Because cattle are corralled overnight, sampling fresh buffalo dung in the morning reduced the chances of inadvertently collecting cattle dung, which is morphologically similar to buffalo dung, although the latter is typically larger and less-well defined (2). To further ensure accuracy, we used DNA minibarcodes to confirm identifications of all putative buffalo samples. We amplified and sequenced a portion of the mitochondrial COI gene from buffalo samples using primers Uni-MinibarF1/C1-N-1777 (Table S1). Reaction mixtures comprised 2.5 mM MgCl<sub>2</sub>, 200 μM each dNTP, 0.1 mg/mL BSA, 4% DMSO, 0.2 μM each primer, AmpliTaq Gold polymerase, and 2 μL DNA (10% dilution) in 12.5 μL. Thermocycling included denaturing at 95°C for 10 min, followed by 5 cycles of 95°C for 1 min, 46°C for 1 min, and 72°C for 30 s, then by 35 cycles with an annealing temperature of 53°C, and ending with a 2 min extension at 72°C. Sequences that overlap this COI region were amplified from cattle samples using primers LCO1490/C1-N-1777 and the same reaction conditions, except that annealing was at 46°C for all 40 cycles (Table S1; the primer Uni-MinibarF1 was unsuccessful on cattle samples while the primer LCO1490 was unsuccessful on buffalo samples). When PCR failed on a putative buffalo sample, we sought to determine if it was instead a cattle sample by repeating PCR using primers LCO1490/C1-N-1777. Amplicons were cleaned using ExoSapIT (Affymetrix) and sequencing was conducted at GeneWiz (South Plainfield, NJ) on an ABI 3730. We obtained DNA minibarcodes from >95% (39 of 41) of putative buffalo samples, confirming their identities and the accuracy of our visual identification. Two incorrectly identified samples (collected together) were reassigned to cattle.

**Laboratory protocols for plant DNA metabarcoding.** We utilized the P6 loop of the chloroplast *trnL*(UAA) region, which can identify a broad array of plant taxa (3). For three plant families that were expected to be frequent in these diets, but for which species-level identifications can be problematic using the *trnL*-P6 marker (Poaceae, Asteraceae, and Cyperaceae), we also sequenced family-specific internal transcribed spacer 1 (ITS) ribosomal DNA markers (4, 5). For the *trnL*-P6 marker, we performed 20 μL reactions comprising 2.5 mM MgCl<sub>2</sub>, 200 μM each dNTP, 0.1 mg/mL BSA, 4% DMSO, 0.2 μM each primer [*trnL*(UAA)g/*trnL*(UAA)h], AmpliTaq Gold polymerase, and 2 μL of DNA extract.

Thermocycling followed a program of initial denaturing at 95°C for 10 min, followed by 35 cycles of 95°C for 30 s, 55°C for 30 s, and 72°C for 30 s, with a 2-min final extension at 72°C. We used the same reaction mixtures for ITS, except that we also performed a multiplex reaction to amplify each of the three ITS targets by mixing 0.3 μM of the forward primer (ITS1-F) with 0.1 μM of each of the three family-specific reverse primers (ITS1Poa-R = Poaceae, ITS1Ast-R = Asteraceae, and ITS1Cyp-R = Cyperaceae; Table S1)(4). Thermocycling followed a program of initial denaturing at 95°C for 10 min, followed by 35 cycles of 94°C for 30 s, 58°C for 30 s, and 72°C for 45 s, with a 2-min final extension at 72°C.

We tagged the 5' end of each DNA metabarcoding primer with an 8-nt multiplex identification (MID) tag that differed by 4-nt from any other tag, thus enabling pooling of up to 96 uniquely identifiable PCR products for sequencing. We used SequalPrep 96-well plates to normalize uniquely tagged PCR products. We then pooled PCR products and concentrated them with Zymo Clean and Concentrator kits. At Princeton University's Lewis Sigler Institute, ~100 ng of DNA from each pool was converted to an Illumina sequencing library using the Apollo 324TM NGS Library Prep System and PrepX DNA kit (Wafergen, CA), which included DNA end-repairing, A-tailing, adapter ligation, and limited amplification. Different Illumina barcodes were ligated to each pool to enable demultiplexing. Library size distributions were quality-checked (Bioanalyzer DNA HS chips, Agilent, CA), quantified (Qubit fluorometer, Invitrogen, CA), pooled at equal amounts, and sequenced on the Illumina HiSeq 2500 Rapid Flowcell as single-end 170 nt reads along with 7 nt index reads (Illumina, CA). The resulting metabarcode sequences were demultiplexed for use in diet analysis (see Text S3, below).

## Text S2. Constructing a plant DNA reference library for Mpala Research Centre, Kenya.

**Reference plant collections and vouchers.** To identify dietary plant sequences obtained from fecal samples, we constructed an extensive DNA reference library of plants occurring throughout Mpala Research Centre and Conservancy. Fertile plant material was collected and voucher specimens were deposited at the National Museums of Kenya and Smithsonian Institution for identification and storage. As part of our ongoing effort to comprehensively catalog and DNA barcode the plant species of Mpala, we have archived these collections and associated DNA data in the Barcode of Life Datasystem (BOLD)(6). To date, the collection includes 1,369 specimens representing ≥291 species (of ~480 species recorded from this region: [http://www.mpala.org/documents/Flora\\_and\\_Fauna\\_2\\_2185861024.pdf](http://www.mpala.org/documents/Flora_and_Fauna_2_2185861024.pdf)). We will continue to update our BOLD database with newly vouchered specimens and expert determinations of provisionally identified specimens. To date, we have identified >99% specimens to family-level, 95% to genus-level, and 80% to species-level. In our analysis, we included all specimens identified to family-level or better, noting that DNA metabarcodes may match specimens that are pending identification.

**Laboratory protocols for plant DNA barcoding.** To facilitate plant identification, we extracted DNA and sequenced three standard plant DNA barcode loci (*matK*, *rbcL*, and *psbA-trnH*) using established primers and protocols (Table S1)(7, 8). We further sequenced chloroplast *trnL*(UAA) and nuclear ITS1, which are gene regions that contain the smaller DNA metabarcode gene regions utilized in this study: *trnL*-P6 and ITS, respectively (Table S1). We sequenced *trnL*(UAA) and ITS1 in separate 12.5 uL PCR reactions that included 2.5 mM MgCl<sub>2</sub>, 200 μM of each dNTP, 0.1 mg/mL BSA, 4% DMSO, 0.2 μM of each primer [*trnL*(UAA)c/*trnL*(UAA)d and ITS-A/ITS-C, respectively], NEB Taq polymerase, and 2 μL DNA extract. Thermocycling for ITS1 included initial denaturing at 95°C for 2 min, followed by 35 cycles of 95°C for 30 s, 55°C

for 30 s, and 72°C for 45 s, with a 5-min final extension at 72°C, whereas the *trnL*(UAA) protocol proceeded at 95°C for 4 min, 35 cycles of 94°C for 30 s, 50°C for 30 s, and 72°C for 1 min, with a 5-min final extension at 72°C. Amplicons were cleaned using ExoSapIT and sequenced using an ABI 3730 at GeneWiz.

### Text S3. DNA metabarcode demultiplexing, quality control, and species identification.

Sequence demultiplexing, quality control, and preliminary identifications were performed using *obitools* (<http://metabarcoding.org/obitools>). We used the *ngsfilter* command to identify sequences by locus and sample, based on two criteria: (a) 100% matches to MID tags and (b) no more than two mismatches with primers. Sequences with nucleotide ambiguities or mean Illumina fastq quality scores <30 across the head, tail, or total length of the sequence were dropped. We used the *obiuniq* command to group identical sequences and tally them within samples, enabling us to quantify the relative read abundance (RRA) of each sequence (Text S4). Sequences that occurred ≤1000 times overall, or that were ≤10 bp for *trnL*-P6 or ≤30 bp for ITS, were discarded. We considered sequences to be likely PCR artifacts if they were highly similar to another sequence (1 bp difference) and had a much lower abundance (0.05%) in the majority of samples in which they occurred; we discarded these using the *obiclean* command. We further eliminated potential chimeras, PCR and sequencing errors, and low-template-quality samples by sequentially removing sequences with poor matches to reference DNA data (≤95% or 99% identity for *trnL*-P6 or ITS markers, respectively) and low per-sample read frequency (≤0.01). Finally, we excluded fecal samples with a low final sequence count (<1,000).

We constructed reference plant DNA libraries using the *ecoPCR* command to extract *trnL*-P6 and ITS sequences from (a) our plant DNA database from Mpala (Text S2) and (b) the global European Molecular Biology Laboratories (EMBL) database (release 118). The locally collected reference database yielded 197 unique *trnL*-P6 sequences from the 1,136 plant specimens from which we successfully sequenced *trnL*(UAA); 77% of the sequences in this subset represented single species/morphospecies, indicating that our metabarcode data can yield fine-scale identifications for most plant taxa in the community. We likewise constructed local reference libraries for each of the three family-specific ITS markers: from 184 Poaceae specimens, we obtained 50 unique sequences, only seven of which could match multiple species or morphospecies; from 80 Asteraceae specimens, we obtained 22 unique sequences, only three of which matched multiple species or morphospecies; from eight Cyperaceae specimens, we obtained three unique sequences, only one of which had been identified to species-level.

We identified dietary sequences using the *ecoTag* command, inspecting and revising taxonomic assignments to ensure validity (Table S3 for *trnL*-P6; Table S7 for ITS). First, we assigned species identities to DNA metabarcode sequences with exact matches (100% identity) to reference sequences; when a dietary sequence exactly matched multiple reference sequences, we revised assignments to the finest taxonomic level that encompassed all matching sequences. Second, we used *ecoTag* to identify the finest taxonomic level that encompassed all DNA sequences when no exact match was made. All sequences were identified at least to family-level; some could not be identified to genus, resulting in matches to sub-familial clades (e.g., the PACMAD clade of Poaceae that contains all C<sub>4</sub> grasses; Tables S3,S7). Third, if percent identity was identical to different taxa in the local and EMBL databases, we gave preference to the local database (13 instances for *trnL*-P6 and 6 for ITS; Tables S3 and S7, respectively). In some cases a sequence matched a taxon in EMBL with a native range that is not known to include Kenya;

we noted such instances (Table S3,S7). Finally, we discarded sequences from ITS datasets that were assigned to a plant family other than the one targeted by the family-specific marker.

#### Text S4. Quantification of DNA metabarcode relative read abundance (RRA).

Sequence read relative abundance (RRA) is defined as the proportion of unique Illumina sequence reads in a sample divided by the final number of sequence reads (i.e., post-quality control) in that sample. We quantified RRA of dietary sequences to (a) provide insight into the relative amount of different plant types in diets and (b) assess whether RRA-based inferences differed qualitatively from those obtained using occurrence-based (i.e., presence/absence) data.

**Cross-validating plant family-level RRA comparisons with stable isotopes.** Evidence suggests that RRA can reflect the quantitative consumption patterns of LMH, at least for coarsely circumscribed plant groups (9), but this has not yet been extensively validated. We assessed the robustness of RRA for comparisons of grass:browse consumption by comparing proportional grass (family Poaceae) representation in samples (mean RRA) with estimates of proportional C<sub>4</sub>-plant representation inferred from fecal stable carbon isotopes. Numerous studies have used stable carbon isotopes to quantify proportional intake of grasses by LMH in African savannas, where the C<sub>4</sub> photosynthetic pathway used by Afro-tropical grasses produces a distinct isotopic signature from that of other plants (e.g., 10, 11, 12). (There are some exceptions to this rule, such as non-grasses with C<sub>4</sub> photosynthesis, but none of the known exceptions in our study area occurred frequently in LMH diets.) We compared mean Poaceae RRA for each LMH species with isotopic estimates of proportional C<sub>4</sub> consumption drawn from (a) a subset of the same fecal samples used for DNA metabarcoding and (b) prior studies from sub-Saharan Africa.

When collecting fecal DNA samples, we simultaneously saved fecal samples for stable-isotope analysis. We also collected leaf tissue from five individuals of four common plant species (C<sub>4</sub> grasses *Cynodon plectostachyus* and *Digitaria milanjiana*, C<sub>3</sub> forb *Solanum campylacanthum*, and C<sub>3</sub> tree *Acacia brevispica*) to serve as end-members in a two-source isotopic mixing model. Samples were dried to constant weight at 72°C (as stipulated by USDA APHIS permit #122489), stored with desiccant, and transported to Princeton University. Prior to fecal sample preparation, we applied an additional 1-hour heat-shock treatment in a 130°C oven as a precaution against the Q fever bacterium *Coxiella burnetii*, which is endemic at our study site. To test for potential effects of this treatment on isotopic results, we collected five fecal samples from each of three domestic LMH on New Jersey farms (horse, *Equus ferus*; sheep, *Ovis aries*; and cattle, *Bos taurus*), as analogs for our study species; because Q fever is not endemic in New Jersey, a portion of each of these samples could be dried at 72°C only, while the remainder were dried and heat-shocked as for the Kenyan samples. Samples from each species (N = 4-5) were homogenized with a mortar and pestle in liquid N<sub>2</sub>, weighed into tin boats (~3 mg), and analyzed for δ<sup>13</sup>C and δ<sup>15</sup>N at the University of California Santa Cruz Stable Isotope Facility (Dumas combustion in a Carlo Erba 1108 elemental analyzer coupled to a ThermoFinnigan Delta Plus XP isotope ratio mass spectrometer).

After applying the paired heat treatments to LMH dung from New Jersey farms, δ<sup>13</sup>C values did not differ between treatment groups (paired *t*-test: *t* = -1.39, df = 14, *P* = 0.19), so we proceeded with analysis of our heat-treated Kenyan samples. We ran one duplicate sample for each LMH and plant species, which demonstrated low instrumental error (δ<sup>13</sup>C differed by <0.1‰ for duplicate plant samples and <0.5‰ for duplicate LMH samples). The dung of LMH species differed significantly in δ<sup>13</sup>C signatures (Table S4). We excluded one Grevy's zebra sample from this and subsequent isotopic analyses because it came from a foal and had radically

outlying  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  values, perhaps due to a largely milk-based diet. We used a two-source carbon-isotope mixing model to estimate the proportion C<sub>4</sub> in samples with the Stable Isotope Analysis in R (SIAR) software (13). We parameterized C<sub>3</sub>- and C<sub>4</sub>-source end members based on the local plant samples ( $\delta^{13}\text{C} = -27.63\% \pm 0.36 \text{ SD}$  and  $-14.14\% \pm 0.10 \text{ SD}$  for C<sub>3</sub> and C<sub>4</sub> end points, respectively), which closely matched values used in prior analyses (11, 14). We assumed tissue-enrichment factors based on the mean diet-to-feces fractionations measured in six mammalian herbivores fed fixed C<sub>3</sub>/C<sub>4</sub> diets in a prior study (15)(0.6 ± 0.3 and 1.4 ± 0.3 for C<sub>3</sub> and C<sub>4</sub> sources, respectively), which closely correspond to values used in prior fecal analyses of African LMH (11, 12, 14).

We tested for correlations between (a) the RRA of grasses and corresponding  $\delta^{13}\text{C}$  values measured from the same samples and (b) the mean grass RRA from the subset of samples from each LMH species used in the SIAR analysis of proportional C<sub>4</sub> consumption. We concluded that family-level inferences of proportional grass consumption based on RRA of our *trnL-P6* metabarcode data are likely to be reliable because they were consistent with stable isotope values.

**Comparing sequence-level occurrence- and RRA-based metrics.** We found a positive correlation between occurrence- and RRA-based metrics of species-level niche breadth ( $t = 2.52$ ,  $\text{df} = 5$ ,  $R^2 = 0.53$ ,  $P = 0.05$ ; Table 1). Likewise, we found a strong correlation between occurrence- and RRA-based measures of interspecific niche overlap (Mantel  $r = 0.911$ ,  $P = 0.001$ ; Table 1). Occurrence-based measures of interspecific dietary dissimilarities were lower than RRA-based dissimilarity measures, suggesting that occurrence provides the more conservative measure with regard to dietary niche partitioning (Table 1). Bipartite networks based on mean RRA show that plant taxa with a high relative frequency of occurrence (FOO) also exhibited high RRA (compare Table S3 and Fig. S6A,B).

Diet composition varied as a function of LMH body mass when compared using RRA-based dissimilarity metrics (*adonis*: pseudo- $F_{1,290} = 27.0$ ,  $R^2 = 0.09$ ,  $P \leq 0.0001$ ; compare Fig. S6C with Fig. 3). This relationship between body mass and diet remained statistically significant (*adonis*: pseudo- $F_{1,288} = 33.3$ ,  $R^2 = 0.09$ ;  $P \leq 0.0001$ ) when considering feeding guild (*adonis*: pseudo- $F_{1,288} = 47.5$ ,  $R^2 = 0.12$ ,  $P \leq 0.0001$ ) and the body mass\*guild interaction (*adonis*: pseudo- $F_{1,288} = 21.7$ ,  $R^2 = 0.06$ ,  $P \leq 0.0001$ ). Considerable dietary niche partitioning among LMH species was also evident using RRA (*adonis*: pseudo- $F_{6,285} = 33.8$ ,  $R^2 = 0.42$ ,  $P \leq 0.0001$ ; Fig. S6D). Collectively, these analyses show that our conclusions are qualitatively consistent using both RRA and occurrence-based metrics.

#### Text S5. Daily movements of GPS-collared zebra.

We quantified daily movements of six zebra (four *Equus grevyi* and two *E. quagga*) using GPS telemetry. Zebras were collared using custom-made GPS-GSM Savannah Tracking Collars as part of a different study by D.I.R. We analyzed movement data from a period close to sample collection (March 31 – May 31, 2014), with animal locations recorded at 15-minute intervals, to determine the mean daily area over which zebra foraged. The mean gastrointestinal retention time (from consumption to defecation) for Grevy's zebra is approximately one day [25 h ± 8.5 SD for solutes, 28 h ± 7.2 SD for particles (16)]. Thus, the area covered by an individual over one day roughly encompasses the range of potential food plants that could be contained in a fecal sample, and samples collected from within an area of that size are likely to have been deposited by individuals foraging within similar plant communities. Zebras of both species ranged over similar distances during the course of our study, moving an average of 11.2 km per

day (range = 8.2 – 14.8 for Grevy’s; 9.7 – 10.6 for plains), encompassing minimum convex polygons with average area of 545 ha (range = 247 – 1,121 for Grevy’s; 478 – 489 for plains) and approximate circular diameters of 2.3 km (Table S5). We therefore used a distance threshold of 2.3 km to analyze subsets of samples from individuals that likely had foraged in similar habitats and encountered similar relative availability of different plant species (see Main Text). We also used this value for buffalo and cattle, for which no movement data were available.

#### **Text S6. Assessing the robustness of the *trnL*-P6 marker using family-specific ITS markers.**

To evaluate the reliability of our conclusions based on *trnL*-P6, we used family-specific ITS metabarcode markers (Text S3), which should provide greater species-level taxonomic resolution of plant sequences within the Poaceae, Asteraceae, and Cyperaceae (5, 17). It is necessary to analyze data separately for ITS and *trnL*-P6 markers because each has different coverage (i.e., breadth of taxa that can be amplified), specificity (i.e., ability to identify sequences above or below the species-level), and biases (e.g., amplification bias due to primer mismatching). Thus, we used the ITS data to independently validate conclusions based on *trnL*-P6 about the relative dietary importance of species within each of the three plant families. To do this, we analyzed bipartite networks and dietary dissimilarity using occurrence-based metrics.

The grasses most frequently detected by ITS, including *Pennisetum* spp., were also frequently detected by *trnL*-P6 (Tables S3,S7). However, some grasses frequently detected by *trnL*-P6 (e.g., *Cynodon plectostachyus*; Table S3) were not detected by ITS (Table S7; Fig. S7A). Surprisingly, ITS revealed high FOO of some grasses in dik-dik diets: at least one grass sequence was detected in 100% of samples (Table S1), with >90% FOO of the top two grass sequences (Table S7). This might be a result of (a) biased PCR amplification of higher-abundance templates using *trnL*-P6 (i.e., grasses have relatively low abundance in dik-dik diets), (b) differences in nuclear vs. chloroplast grass DNA abundance, and/or (c) greater read depth of Poaceae-specific ITS than *trnL*-P6 (Table S2). The grasses in dik-dik diets had greater overlap with those in mixed-feeder (impala, elephant) diets than those in grazer diets (Fig. S7A). Although the extent of the dietary niche partitioning of grasses inferred from the Poaceae-specific ITS marker was lower than that observed for all taxa using the *trnL*-P6 marker, we found significant differences among LMH species using ITS, which were qualitatively similar to those obtained using *trnL*-P6 (*adonis*: pseudo- $F_{6,286} = 28.3$ ,  $R^2 = 0.37$ ,  $P \leq 0.0001$ ; Fig. S7B).

In this grass-specific ITS-based analysis, intraspecific sequence diversity may occur for several plant taxa (Table S7) and artificially increase the dissimilarity measured among samples within LMH species. For example, *Eragrostis papposa* and *Brachiaria deflexa* both yielded 100% matches to >1 dietary sequences, which differed in FOO among LMH species (Table S7). Merging unique sequences that matched a single plant taxon within LMH samples resulted in a minor increase in the effect size of dietary niche partitioning (*adonis*: pseudo- $F_{6,286} = 28.8$ ,  $R^2 = 0.38$ ,  $P \leq 0.0001$ ). To a lesser extent, similar intraspecific diversity may also occur within the *trnL*-P6 dataset (e.g., *Pennisetum* spp.; Tables S3,S7). However, as observed in this grass-specific ITS analysis, such variation should only diminish the niche-partitioning signal. Species-level botanical determinations of grass specimens from our Mpala reference collection that are currently awaiting review by experts will further improve the precision of this analysis.

The Asteraceae-specific ITS marker also yielded results consistent with those found using *trnL*-P6. The most frequently detected asters, including *Hirpicium diffusum* and *Gutenbergia* spp., were relatively frequent in the diets of elephants, impala, dik-dik, and cattle, whereas no aster was detected with high frequency in the diets of either zebra or buffalo (Fig.

S7C). The ITS analysis indicated substantial overlap in use of plants from this family between cattle and the three non-grazers (Fig. S7C), paralleling the indication from *trnL*-P6 that cattle diets overlap as much with traditionally defined grazer species as they do with traditionally defined non-grazer species (Table 1). The asters detected using the ITS marker differed significantly among LMH species (*adonis*: pseudo- $F_{6,130} = 8.38$ ,  $R^2 = 0.28$ ,  $P \leq 0.0001$ ). Aster sequences were more frequently detected in dik-dik samples than in samples of any other LMH species, and inter-individual variation was considerable among them (Table S2; Fig. S7D).

The Cyperaceae-specific ITS marker yielded no exact match to Cyperaceae sequences in the reference database, although an abundance of sequences from non-target plant families suggests the fidelity of these primers for Cyperaceae DNA templates may be low. With a >95% identity threshold, only two sequences from nine samples were obtained using the Cyperaceae-specific ITS markers (Table 2). Thus, differences between the ITS and *trnL*-P6 markers in the detectability of plants in this family would not significantly alter our results (Tables S3,S7).

In summary, the three ITS markers provide independent evidence that suggests our results are not highly sensitive to the limited specificity and/or potential amplification biases of the broad-spectrum *trnL*-P6 marker, and thus that our conclusions are robust. Dietary profiles were qualitatively consistent across both markers, despite technical limitations inherent to each.

## References in Supporting Information

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**Table S1.** Primers utilized in this study.

Primer	Sequence	Reference
C1-N-1777	ACTTATATTGTTATACGAGGGAA	(18)
ITS-A	GGAAGGAGAAGTCGTAACAAGG	(19)
ITS-C	GCAATTCACACCCAAGTATCGC	(19)
ITS1-F	GATATCCGTTGCCGAGAGTC	(5)
ITS1Ast-R	CGGCACGGCATGTGCCAAGG	(5)
ITS1Cyp-R	GGATGACGCCAAGGAACAC	(17)
ITS1Poa-R	CCGAAGGCGTCAAGGAACAC	(5)
rbcLa-F	ATGTCACCACAAACAGAGACTAAAGC	(20)
rbcLa-R	ATGTCACCACAAACAGAGACTAAAGC	(21)
matK-xf	TAATTTACGATCAATTCAATT	(22)
matK-MALP	ACAAGAAAGTCGAAGTAT	(23)
matK-1RKIM-f	ACCCAGTCCATCTGGAAATCTTGGTTC	Ki-Joong Kim, pers. comm.
matK-3FKIM-r	CGTACAGTACTTTGTGTTACGAG	Ki-Joong Kim, pers. comm.
psbA3-f	GTTATGCATGAACGTAATGCTC	(24)
trnL(UAA)c	CGAAATCGGTAGACGCTACG	(25)
trnL(UAA)d	GGGGATAGAGGGACTTGAAC	(25)
trnL(UAA)g	GGGCAATCCTGAGCCAA	(3)
trnL(UAA)h	CCATTGAGTCTCTGCACCTATC	(3)
trnHR	GAACGACGGATTGAAC	(24)
LCO1490	GGTCAACAAATCATAAGATATTGG	(26)
Uni-MinibarF1	TCCACTAATCACAARGATATTGGTAC	(27)

**Table S2.** Sample sizes and numbers of sequences at key stages in the analysis. Family-specific ITS markers are signified by the first three letters of each family (Asteraceae = ITS-Ast; Cyperaceae = ITS-Cyp; Poaceae = ITS-Poa).

	<b>Marker</b>	<b>Buffalo</b>	<b>Cattle</b>	<b>Dik-Dik</b>	<b>Elephant</b>	<b>Grevy's</b>	<b>Impala</b>	<b>Plains</b>
Fecal samples analyzed	Both	39	52	47	27	39	48	41
High quality sequence reads	<i>trnL</i> -P6	904,058	734,943	845,875	446,558	387,893	566,179	436,981
	ITS-Ast	18,968	262,236	2,351,560	556,694	13,843	1,096,130	14,348
	ITS-Cyp	70,498	82,231	75,150	384,666	137,160	38,884	73,536
	ITS-Poa	2,663,441	3,354,647	2,308,587	1,917,662	2,324,895	3,417,551	3,452,295
Final # samples	<i>trnL</i> -P6	39	52	46	27	39	48	41
	ITS-Ast	1	29	39	20	1	45	2
	ITS-Cyp	2	0	0	5	1	0	1
	ITS-Poa	39	52	47	27	39	48	41
Final # unique sequences	<i>trnL</i> -P6	62	54	45	46	40	60	32
	ITS-Ast	3	6	12	9	4	7	2
	ITS-Cyp	1	0	0	2	1	0	1
	ITS-Poa	29	28	24	21	26	21	28

**Table S3.** Identification of *trnL*-P6 dietary sequences and their relative frequency of occurrence (FOO) in samples from each LMH species. Sequence information for each *trnL*-P6 metabarcode sequence includes the best match (% identity expressed as a proportion) to a reference sequence in the local Mpala or EMBL database (including references to BOLD Process IDs in the archived local reference library and EMBL accession numbers, respectively). Sequences are identified to family or better. When exact matches were made to multiple taxa, assignments were adjusted to the next-highest taxonomic level (shown in parentheses) and each matching species is listed in brackets. Representative BOLD Process ID numbers are given in parentheses for exact matches to morphospecies that have not been identified to species-level. In cases where exact matches in the EMBL database were to species that may not occur in Kenya, we provide that species' known distribution in brackets. When no exact match was made to either database, the finest taxonomic level including all best-matching taxa is given in parentheses.

Seq.	Sequence Information				Family	Best Identity	Frequency of Occurrence							
	Local	EMBL	Local	EMBL			Buffalo	Cattle	Dik-Dik	Elephant	Grevy's	Impala	Plains	Total
P6_020	1.00	0.98	UHURU575-14	EF196918	Poaceae	<i>Cynodon plectostachyus</i> <i>Digitaria</i> (genus) [ <i>Digitaria milanjiana</i> ; <i>Digitaria velutina</i> ; <i>Digitaria</i> spp. (UHURU429-14; UHURU1262-15)]	0.90	0.98	0.00	1.00	0.95	0.96	0.66	0.76
P6_024	1.00	0.98	MIXED016	EU056305	Poaceae	<i>Cynodonteae</i> (tribe) <i>Indigofera</i> (genus) [ <i>Indigofera circinella</i> ; <i>Indigofera hochstetteri</i> ]	0.97	1.00	0.02	0.33	0.77	0.90	0.76	0.70
P6_025	0.96	0.94	UHURU575-14	EF196918	Poaceae	<i>Pennisetum stramineum</i> *	0.46	0.96	0.04	0.78	1.00	0.98	0.66	0.70
P6_017	1.00	0.98	MIXED044	AF274360	Fabaceae	<i>Pennisetum mezanum</i> *	0.85	1.00	0.87	0.30	0.33	0.98	0.02	0.66
P6_021	1.00	0.98	UHURU978-14	DQ890472	Poaceae	<i>Acacia brevispica</i>	1.00	0.50	0.00	0.59	0.97	0.44	0.98	0.62
P6_008	1.00	0.98	UHURU602-14	EU939989	Poaceae	<i>Andropogonea</i> (tribe) [ <i>Bothriochloa insculpta</i> ; <i>Cymbopogon commutatus</i> ; <i>Hyparrhenia anamesa</i> ; <i>Hyparrhenia</i> sp. aff. <i>Nubica</i> ]	0.56	0.69	0.00	0.19	0.87	0.04	0.95	0.47
P6_026	1.00	0.98	UHURU026-14	JX870569	Fabaceae	<i>Indigofera</i> (genus)	0.59	0.23	0.70	1.00	0.03	0.81	0.00	0.46
P6_022	1.00	0.98	MIXED004	EF156683	Poaceae	<i>Acacia drepanolobium</i> ; <i>Acacia etbaica</i> ; <i>Acacia gerrardii</i> ; <i>Acacia tortilis</i>	0.69	0.65	0.00	0.07	0.56	0.08	1.00	0.45
P6_007	0.98	0.96	UHURU1337-15	AF274360	Fabaceae	<i>Acacia</i> (genus) [ <i>Acacia</i> <i>drepanolobium</i> ; <i>Acacia etbaica</i> ; <i>Acacia gerrardii</i> ; <i>Acacia tortilis</i> ]	0.46	0.85	0.37	0.04	0.08	0.69	0.00	0.40
P6_003	1.00	0.98	MIXED001	FJ009898	Fabaceae		0.15	0.08	0.93	0.93	0.00	0.71	0.00	0.38

P6_042	0.96	0.94	UHURU602-14	AY769175	Poaceae	PACMAD clade PACMAD clade [ <i>Dinebra retroflexa</i> ; <i>Enteropogon macrostachyus</i> ; <i>Melinis repens</i> ; <i>Microchloa kunthii</i> ] Malvaceae (family) [ <i>Hibiscus calyphyllus</i> ; <i>Malva parviflora</i> ] PACMAD clade [ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)] Paniceae (tribe)	0.36	0.75	0.00	0.19	0.72	0.08	0.46	0.37
P6_035	1.00	0.98	MIXED017	AY769175	Poaceae	[ <i>Dinebra retroflexa</i> ; <i>Enteropogon macrostachyus</i> ; <i>Melinis repens</i> ; <i>Microchloa kunthii</i> ] Malvaceae (family) [ <i>Hibiscus calyphyllus</i> ; <i>Malva parviflora</i> ] PACMAD clade [ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)] Paniceae (tribe)	0.38	0.65	0.00	0.48	0.69	0.13	0.24	0.36
P6_011	1.00	1.00	MIXED021	HQ696727	Malvaceae	[ <i>Hibiscus calyphyllus</i> ; <i>Malva parviflora</i> ] PACMAD clade [ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)] Paniceae (tribe)	0.62	0.29	0.61	0.07	0.00	0.65	0.05	0.35
P6_051	1.00	0.98	MATCHS38	AY116259	Poaceae	[ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)] Paniceae (tribe)	0.36	0.12	0.00	0.33	0.64	0.15	0.90	0.34
P6_001	1.00	0.98	MIXED005	GU594587	Poaceae	[ <i>Brachiaria lachnantha</i> ; <i>Panicum maximum</i> ; <i>Urochloa brachyura</i> ] Acacia mellifera	0.87	0.31	0.00	0.52	0.15	0.10	0.44	0.32
P6_006	1.00	0.98	UHURU1222-15	AF522975	Fabaceae	<i>Themeda triandra</i>	0.03	0.00	0.63	0.59	0.00	0.85	0.02	0.30
P6_033	1.00	0.96	UHURU890-14	EF156683	Poaceae	<i>Pentanisia ouranogyne</i>	0.62	0.19	0.00	0.00	0.31	0.00	0.98	0.29
P6_058	1.00	0.96	UHURU470-14	AM266936	Rubiaceae	PACMAD clade [Poaceae sp. (UHURU1242-15)] Chloridoideae	0.36	0.58	0.20	0.00	0.03	0.48	0.02	0.27
P6_049	1.00	0.98	UHURU1242-15	AY116262	Poaceae	(subfamily) [ <i>Eragrostis papposa</i> ; <i>Eragrostis racemosa</i> ; <i>Sporobolus ioclados</i> ] <i>Phyllanthus</i> (genus)	0.28	0.19	0.00	0.04	0.33	0.04	0.73	0.23
P6_014	1.00	0.98	MIXED019	DQ655886	Poaceae	[ <i>Phyllanthus sepialis</i> ; <i>Phyllanthus</i> sp. (UHURU699-14)]	0.00	0.31	0.00	0.00	0.59	0.17	0.34	0.21
P6_034	1.00	0.96	MATCHS10	FJ847837	Phyllanthaceae	<i>Harpachne schimperi</i>	0.31	0.38	0.22	0.00	0.03	0.31	0.00	0.20
P6_064	1.00	0.98	UHURU556-14	DQ655884	Poaceae		0.00	0.48	0.00	0.04	0.44	0.06	0.24	0.19

P6_037	0.98	0.96	MIXED016	EF156733	Poaceae	Panicoideae (subfamily) <i>Grewia</i> (genus) [ <i>Grewia kakothamnos</i> ; <i>Grewia similis</i> ] <i>Hibiscus</i> (genus) [ <i>Hibiscus micranthus</i> ; <i>Hibiscus meyeri</i> ]	0.92	0.08	0.00	0.11	0.21	0.02	0.10	0.19
P6_043	1.00	0.99	MIXED043	KC479279	Malvaceae		0.21	0.04	0.22	0.26	0.03	0.35	0.05	0.16
P6_012	1.00	0.92	MIXED022	AY328160	Malvaceae	[ <i>Hibiscus micranthus</i> ; <i>Hibiscus meyeri</i> ]	0.13	0.02	0.43	0.22	0.00	0.21	0.00	0.14
P6_019	1.00	0.89	UHURU014-14	AY328160	Malvaceae	<i>Abutilon mauritianum</i> Asteraceae (family) [ <i>Vernonia galamensis</i> ; <i>Gutenbergia boranensis</i> ; <i>Gutenbergia cordifolia</i> ; <i>Kleinia squarrosa</i> ; <i>Solanecio angulatus</i> ; <i>Solanecio cydoniifolius</i> ; Asteraceae sp. (UHURU417-14); <i>Vernonia</i> sp. (UHURU129-14)]	0.49	0.08	0.00	0.44	0.00	0.02	0.00	0.12
P6_040	1.00	0.98	MIXED036	AY216061	Asteraceae	<i>Solanum (genus)</i> [ <i>Solanum campylacanthum</i> ; <i>Solanum coagulans</i> ; <i>Solanum indicum</i> ; <i>Solanum lanzae</i> ; <i>Solanum</i> sp. (UHURU270-14)]	0.05	0.44	0.11	0.00	0.00	0.13	0.00	0.12
P6_073	1.00	0.98	MIXED034	DQ180475	Solanaceae		0.00	0.00	0.02	0.81	0.00	0.23	0.00	0.12
P6_016	1.00	0.98	UHURU605-14	JN249677	Euphorbiaceae	<i>Euphorbia inaequilatera</i> <i>Pennisetum</i> (genus) [ <i>Pennisetum mezianum</i> ; <i>Pennisetum stramineum</i> ]*	0.00	0.13	0.26	0.00	0.00	0.27	0.00	0.11
P6_083	1.00	0.90	MIXED029	EU929058	Poaceae		0.13	0.00	0.00	0.00	0.23	0.15	0.27	0.11
P6_023	1.00	0.87	UHURU596-14	AY328160	Malvaceae	<i>Melhania ovata</i>	0.49	0.13	0.07	0.00	0.00	0.04	0.00	0.11
P6_004	0.96	0.98	UHURU030-14	EF688731	Amaranthaceae	Amaranthaceae (family)	0.00	0.00	0.48	0.00	0.00	0.13	0.00	0.10
P6_059	1.00	0.96	UHURU405-14	DQ172209	Poaceae	<i>Aristida kenyensis</i>	0.03	0.04	0.00	0.00	0.44	0.00	0.15	0.09
P6_078	1.00	0.96	UHURU232-14	DQ655884	Poaceae	<i>Eragrostis</i> sp. (UHURU232-14)	0.00	0.23	0.00	0.04	0.33	0.00	0.00	0.09
P6_053	0.93	0.98	MATCHS38	GQ869932	Poaceae	PACMAD clade	0.26	0.08	0.00	0.00	0.08	0.17	0.02	0.09
P6_015	0.95	1.00	MATCHS38	GQ869934	Poaceae	<i>Garnotia tenella</i> [Known distribution in SE Asia]	0.23	0.04	0.00	0.07	0.03	0.19	0.02	0.08
P6_036	0.98	0.94	UHURU470-14	AM266936	Rubiaceae	<i>Pentanisia</i> (genus)	0.00	0.23	0.15	0.00	0.00	0.06	0.00	0.08

P6_057	1.00	0.96	UHURU118-14	AY328142	Malvaceae	<i>Sida</i> sp. (UHURU118-14)	0.10	0.17	0.00	0.00	0.05	0.10	0.00	0.07
P6_086	1.00	0.98	MIXED008	EF156732	Poaceae	<i>Chloris</i> (genus) [ <i>Chloris virgata</i> ; <i>Chloris gayana</i> ]	0.00	0.12	0.00	0.00	0.28	0.02	0.00	0.06
P6_038	0.99	1.00	MIXED043	KC479279	Malvaceae	<i>Grewia</i> sp.	0.31	0.08	0.02	0.04	0.00	0.00	0.00	0.06
P6_041	0.90	0.98	MATCHS38	GQ869932	Poaceae	<i>Garnotia</i> (genus)	0.44	0.00	0.00	0.00	0.00	0.00	0.00	0.06
P6_013	0.94	0.96	UHURU030-14	EF688731	Amaranthaceae	<i>Achyranthes</i> (genus)	0.00	0.00	0.33	0.00	0.00	0.04	0.00	0.06
P6_048	1.00	1.00	UHURU309-14	DQ655880	Poaceae	<i>Eragrostis superba</i>	0.13	0.12	0.00	0.00	0.08	0.00	0.02	0.05
P6_065	1.00	0.98	UHURU407-14	DQ924225	Ebenaceae	<i>Euclea divinorum</i>	0.08	0.04	0.00	0.07	0.00	0.15	0.00	0.05
P6_077	1.00	0.94	UHURU1288-15	AJ558038	Aizoaceae	<i>Zaleya pentandra</i>	0.00	0.10	0.04	0.15	0.00	0.06	0.00	0.05
P6_066	1.00	0.95	UHURU174-14	EU497701	Euphorbiaceae	<i>Croton dichogamous</i>	0.21	0.04	0.00	0.04	0.00	0.00	0.00	0.04
P6_067	1.00	0.98	UHURU1312-15	AJ875117	Rutaceae	<i>Teclea nobilis</i>	0.03	0.00	0.17	0.00	0.00	0.04	0.00	0.04
P6_027	0.99	0.88	UHURU596-14	AY328160	Malvaceae	<i>Melhania</i> (genus)	0.26	0.00	0.02	0.00	0.00	0.00	0.00	0.04
P6_106	1.00	0.96	UHURU422-14	DQ172209	Poaceae	<i>Aristida congesta</i>	0.00	0.00	0.00	0.00	0.23	0.00	0.02	0.03
P6_115	0.98	0.98	UHURU1233-15	EU939980	Poaceae	PACMAD clade	0.00	0.00	0.00	0.00	0.03	0.08	0.12	0.03
P6_105	0.98	0.98	UHURU1084-14	DQ655886	Poaceae	PACMAD clade	0.03	0.02	0.00	0.11	0.03	0.08	0.00	0.03
P6_056	0.95	0.98	UHURU1312-15	EU326059	Rubiaceae	Rubiaceae (family)	0.00	0.00	0.09	0.00	0.00	0.13	0.00	0.03
P6_089	1.00	0.98	UHURU1309-15	AF127058	Poaceae	<i>Echinochloa pyramidalis</i> Solanaceae (family) [ <i>Lycium europaeum</i> ; <i>Solanum nigrum</i> ; <i>Withania somnifera</i> ]	0.13	0.00	0.00	0.15	0.00	0.00	0.00	0.03
P6_005	1.00	0.98	MIXED027	AY266260	Solanaceae	<i>Ruellia</i> (genus) [ <i>Ruellia patula</i> ; <i>Ruellia prostrata</i> ] <i>Acalypha californica</i> [Known distribution in California, USA]	0.00	0.00	0.07	0.04	0.00	0.10	0.00	0.03
P6_087	1.00	0.98	MIXED033	AB162025	Acanthaceae	<i>Hermannia uhlbergii</i>	0.10	0.06	0.00	0.00	0.00	0.04	0.00	0.03
P6_098	0.91	1.00	UHURU1115-14	AY794776	Euphorbiaceae	<i>Monechma debile</i>	0.00	0.00	0.09	0.00	0.00	0.08	0.00	0.03
P6_010	1.00	0.70	UHURU815-14	HM488394	Malvaceae	<i>Psilotrichum elliotii</i>	0.05	0.00	0.00	0.19	0.03	0.00	0.00	0.03
P6_068	1.00	0.95	UHURU588-14	AF289724	Acanthaceae	<i>Rhynchosia minima</i>	0.13	0.04	0.00	0.00	0.03	0.00	0.00	0.03
P6_110	1.00	0.98	UHURU1013-14	EF688787	Amaranthaceae	<i>Boscia angustifolia</i>	0.00	0.06	0.09	0.00	0.00	0.00	0.00	0.02
P6_039	1.00	0.98	UHURU054-14	AF309858	Fabaceae	<i>Cyathula cylindrica</i>	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.02
P6_084	0.91	0.98	MATCHS38	GQ869932	Poaceae	PACMAD clade	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.03
P6_054	1.00	1.00	UHURU852-14	AY122435	Capparaceae	<i>Cyathula cylindrica</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02
P6_104	1.00	1.00	UHURU681-14	EF688787	Amaranthaceae									

P6_032	1.00	0.98	UHURU439-14	AF141712	Asteraceae	<i>Helichrysum glumaceum</i>	0.00	0.12	0.00	0.00	0.00	0.02	0.00	0.02
P6_117	1.00	0.96	UHURU386-14	AJ387946	Zygophyllaceae	<i>Balanites aegyptica</i>	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.02
P6_076	0.96	0.96	UHURU026-14	AF278531	Fabaceae	<i>Acacia</i> (genus)	0.00	0.00	0.00	0.26	0.00	0.00	0.00	0.02
P6_074	0.98	1.00	UHURU030-14	EF688731	Amaranthaceae	<i>Achyropsis avicularis</i> [Known distribution in South Africa]	0.00	0.00	0.15	0.00	0.00	0.00	0.00	0.02
P6_018	0.78	0.98	UHURU1078-14	AY594496	Anacardiaceae	Anacardiaceae (family)	0.08	0.02	0.00	0.07	0.00	0.02	0.00	0.02
P6_095	1.00	0.98	UHURU1352-15	AF274367	Fabaceae	<i>Indigofera</i> sp. (UHURU1352-15)	0.00	0.02	0.04	0.00	0.00	0.06	0.00	0.02
P6_028	1.00	1.00	UHURU721-14	HE795473	Geraniaceae	<i>Monsonia angustifolia</i>	0.00	0.02	0.04	0.00	0.00	0.06	0.00	0.02
P6_070	1.00	0.98	MIXED002	AF309478	Fabaceae	<i>Acacia</i> (genus) [ <i>Acacia nilotica</i> ; <i>Acacia seyal</i> ; <i>Acacia xanthophloea</i> ]	0.00	0.00	0.07	0.11	0.00	0.00	0.00	0.02
P6_063	0.98	0.96	UHURU054-14	AF309858	Fabaceae	<i>Rhynchosia</i> (genus)	0.08	0.04	0.00	0.00	0.03	0.00	0.00	0.02
P6_009	0.91	1.00	UHURU1217-15	AY792527	Poaceae	<i>Leersia hexandra</i>	0.13	0.00	0.00	0.04	0.00	0.00	0.00	0.02
P6_082	0.98	0.98	UHURU1222-15	AY944539	Fabaceae	<i>Acacia</i> (genus)	0.00	0.00	0.07	0.00	0.00	0.06	0.00	0.02
P6_050	1.00	0.96	MIXED042	EU528915	Acanthaceae	<i>Barleria</i> (genus) [ <i>Barleria eranthemoides</i> ; <i>Barleria ramulosa</i> ; <i>Barleria trispinosa</i> ]	0.00	0.00	0.11	0.00	0.00	0.00	0.00	0.02
P6_118	1.00	0.96	UHURU1293-15	GQ869998	Poaceae	<i>Lintonia nutans</i>	0.05	0.00	0.00	0.00	0.03	0.00	0.05	0.02
P6_116	1.00	0.98	UHURU1233-15	GU594587	Poaceae	<i>Brachiaria deflexa</i>	0.00	0.02	0.00	0.00	0.05	0.04	0.00	0.02
P6_044	1.00	0.98	UHURU1078-14	AY905472	Onagraceae	<i>Ludwigia stolonifera</i>	0.03	0.02	0.00	0.07	0.03	0.00	0.00	0.02
P6_030	1.00	0.98	UHURU030-14	EF688731	Amaranthaceae	<i>Achyranthes aspera</i>	0.13	0.00	0.00	0.00	0.00	0.00	0.00	0.02
P6_055	1.00	0.96	UHURU778-14	EU528915	Acanthaceae	<i>Barleria spinisepala</i>	0.00	0.00	0.00	0.00	0.00	0.08	0.00	0.01
P6_122	1.00	0.95	UHURU1204-15	AJ225792	Rhamnaceae	<i>Scutia myrtina</i>	0.03	0.00	0.02	0.04	0.00	0.02	0.00	0.01
P6_103	1.00	0.98	MIXED039	AF098854	Asteraceae	Asteraceae (family) [ <i>Melanthera scandens</i> ; <i>Sphaeranthus suaveolens</i> ; <i>Sonchus</i> sp. (UHURU268-14)]	0.00	0.00	0.00	0.07	0.00	0.04	0.00	0.01
P6_096	0.98	0.96	UHURU030-14	EF688734	Amaranthaceae	<i>Achyranthes</i> (genus)	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_108	0.98	0.96	UHURU030-14	EF688731	Amaranthaceae	<i>Achyranthes</i> (genus)	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_093	0.88	0.97	MATCHS38	GQ869932	Poaceae	PACMAD clade	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_046	0.89	0.96	UHURU1115-14	JN207679	Euphorbiaceae	<i>Euphorbia</i> (genus)	0.03	0.00	0.07	0.00	0.00	0.00	0.00	0.01
P6_002	1.00	0.93	UHURU921-14	KC420617	Acanthaceae	<i>Dyschoriste radicans</i>	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.01

P6_101	1.00	1.00	UHURU820-14	AB508807	Asparagaceae	<i>Asparagus falcatus</i>	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.01
P6_029	1.00	0.96	UHURU312-14	AY122435	Capparaceae	<i>Cadaba farinosa</i>	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.01
P6_061	1.00	0.98	UHURU1108-14	FJ466473	Burseraceae	<i>Commiphora habessinica</i>	0.05	0.00	0.02	0.00	0.00	0.00	0.00	0.01
P6_112	0.98	0.94	MIXED041	AY328160	Malvaceae	Malvaceae (family)	0.00	0.00	0.04	0.00	0.00	0.02	0.00	0.01
P6_107	0.98	0.96	UHURU1172-14	DQ104308	Poaceae	PACMAD clade	0.00	0.00	0.00	0.00	0.03	0.02	0.02	0.01
P6_120	0.98	0.98	MIXED008	AY523507	Poaceae	Cynodontae (tribe)	0.00	0.00	0.00	0.04	0.00	0.00	0.05	0.01
P6_114	0.96	0.96	UHURU1233-15	EU939980	Poaceae	PACMAD clade	0.00	0.02	0.00	0.07	0.00	0.00	0.00	0.01
P6_045	0.91	1.00	MATCHS38	GQ869932	Poaceae	<i>Garnotia acutigluma</i> [Known distribution in SE Asia]	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_125	0.91	0.98	UHURU310-14	AB445386	Crassulaceae	Crassulaceae (family)	0.00	0.00	0.00	0.00	0.08	0.00	0.00	0.01
P6_080	0.93	0.98	UHURU1108-14	GU246085	Burseraceae	Burseraceae (family)	0.08	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_111	1.00	1.00	UHURU060-14	AF460121	Asteraceae	<i>Aspilia pleuriseta</i>	0.03	0.00	0.00	0.00	0.00	0.00	0.02	0.01
P6_091	1.00	0.98	MIXED011	AY122438	Cleomaceae	<i>Cleome</i> (genus) [ <i>Cleome hirta</i> ; <i>Cleome monophylla</i> ; <i>Cleome</i> sp. (UHURU086-14); <i>Cleome gynandra</i> ]	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.01
P6_081	0.98	0.96	UHURU1222-15	AF522975	Fabaceae	<i>Acacia</i> (genus)	0.00	0.00	0.00	0.00	0.00	0.04	0.00	0.01
P6_060	0.96	0.98	UHURU1352-15	AF274367	Fabaceae	<i>Indigofera</i> (genus) <i>Hibiscus</i> (genus)	0.05	0.00	0.00	0.00	0.00	0.00	0.00	0.01
P6_079	1.00	0.95	MIXED041	AY328160	Malvaceae	[ <i>Hibiscus aponeurus</i> ; <i>Hibiscus flavifolius</i> ]	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00
P6_113	1.00	0.98	UHURU444-14	AY945827	Verbenaceae	<i>Lippia javanica</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
P6_072	1.00	0.98	UHURU378-14	AY122431	Capparaceae	<i>Maerua triphylla</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
P6_090	1.00	0.98	UHURU150-14	AF289724	Acanthaceae	<i>Justicia diclipterooides</i> <i>Ipomoea</i> (genus)	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
P6_094	1.00	0.97	MIXED025	AY101084	Convolvulaceae	[ <i>Ipomoea sinensis</i> ; <i>Ipomoea spathulata</i> ; <i>Ipomoea wightii</i> ]	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
P6_119	0.98	0.98	UHURU681-14	EF688787	Amaranthaceae	Amaranthaceae (family)	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00
P6_099	0.96	0.94	UHURU299-14	HE577609	Amaranthaceae	<i>Chenopodium</i> (genus)	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00
P6_109	0.98	1.00	MIXED002	FJ009877	Fabaceae	<i>Senna gardneri</i>	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
P6_121	0.94	0.96	UHURU1309-15	JQ041837	Poaceae	<i>Digitaria</i> (genus)	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00

\*Possible interspecific variation in the *trnL*-P6 sequence based on the local DNA reference library.

**Table S4.** Measured  $\delta^{13}\text{C}$  values and estimated proportional C<sub>4</sub> intake by each species from stable isotope analysis of fecal samples collected at Mpala Research Centre in 2013 (a subset of the samples used for DNA metabarcoding). Tukey's HSD indicates significant pairwise differences between species in  $\delta^{13}\text{C}$  values (ANOVA:  $F_{6,26} = 33.7$ ,  $P < 0.001$ ). Mean residual error values reflect intraspecific variation in the outputs of the SIAR model.

Samples		$\delta^{13}\text{C}$			Proportion C <sub>4</sub>		
Species	N	Mean	SD	Tukey HSD	Mean	SD	Mean residual error
Plains zebra	5	-13.83	0.52	A	0.92	0.04	0.67
Grevy's zebra	3	-14.50	0.10	A	0.86	0.08	1.64
Buffalo	5	-14.57	0.45	A	0.87	0.04	0.63
Cattle	5	-14.61	0.45	A	0.87	0.04	0.63
Impala	5	-21.91	4.59	B	0.41	0.15	6.60
Elephant	5	-23.26	2.94	B	0.31	0.12	4.32
Dik-Dik	5	-28.26	0.49	C	0.04	0.06	2.52

**Table S5.** Daily movement patterns of GPS-collared zebra at Mpala Research Centre.

Focal zebra	Species	Days	Distance moved (km)			Minimum convex polygon (ha)			Circle diameter (km)		
			Mean	Min	Max	Mean	Min	Max	Mean	Min	Max
Grevy's	Grevy's	93	14.8	7.3	25.4	609.3	108.4	2,037.9	2.7	1.2	5.1
Grevy's	Grevy's	93	9.7	3.7	19.8	323.9	27.2	167.0	1.9	0.6	4.6
Grevy's	Grevy's	93	8.2	2.1	20.1	247.2	11.0	1,862.0	1.6	0.4	4.9
Grevy's	Grevy's	93	13.9	2.3	32.5	1,121.4	28.7	8,617.5	3.2	0.6	10.5
Plains	Plains	80	10.6	1.1	22.2	488.8	6.1	2,557.6	2.3	0.3	5.7
Plains	Plains	32	9.7	1.0	18.9	477.8	4.6	1,236.9	2.3	0.2	4.0
Mean		80.7	11.2	2.9	23.2	544.7	31.0	2,996.9	2.3	0.6	5.8

**Table S6.** Indicator species analysis for the diets of equids (plains vs. Grevy's zebras) and bovines (buffalo vs. cattle). The table is organized with the zebra-zebra comparison presented first and the buffalo-cattle comparison presented last. For plant taxa occurring in the diets of each species pair (sequence information and taxon identification described as in Table S3), comparisons indicate differences in frequency of occurrence (FOO) between the two focal species. *P*-values indicate significant differences, with "NS" signifying  $P > 0.05$ .

Sequence Information			Taxon Identification			Comparison		
Seq.	Local	EMBL	Family	Best Identity		Grevy's FOO	Plains FOO	<i>P</i> -value
P6_021	UHURU978-14	DQ890472	Poaceae	<i>Pennisetum stramineum</i>		0.97	0.98	NS
P6_008	UHURU602-14	EU939989	Poaceae	<i>Pennisetum meianum</i>		0.87	0.95	NS
P6_025	UHURU575-14	EF196918	Poaceae	Cynodontae (tribe)		1.00	0.66	0.00
P6_020	UHURU575-14	EF196918	Poaceae	<i>Cynodon plectostachyus</i>		0.95	0.66	0.00
P6_022	MIXED004	EF156683	Poaceae	Andropogonea (tribe) [ <i>Bothriochloa insculpta</i> ; <i>Cymbopogon commutatus</i> ; <i>Hyparrhenia anamesa</i> ; <i>Hyparrhenia</i> sp. aff. <i>Nubica</i> ] PACMAD clade [ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)]		0.56	1.00	0.00
P6_051	MATCHS38	AY116259	Poaceae	<i>Digitaria</i> (genus) [ <i>Digitaria milanjiana</i> ; <i>Digitaria velutina</i> ; <i>Digitaria</i> spp. (UHURU429-14; UHURU1262-15)]		0.64	0.90	0.02
P6_024	MIXED016	EU056305	Poaceae	<i>Themeda triandra</i>		0.77	0.76	NS
P6_033	UHURU890-14	EF156683	Poaceae	PACMAD clade		0.31	0.98	0.00
P6_042	UHURU602-14	AY769175	Poaceae	PACMAD clade [Poaceae sp. (UHURU1242-15)]		0.72	0.46	0.04
P6_049	UHURU1242-15	AY116262	Poaceae	PACMAD clade [ <i>Dinebra retroflexa</i> ; <i>Enteropogon macrostachyus</i> ; <i>Melinis repens</i> ; <i>Microchloa kunthii</i> ]		0.33	0.73	0.00
P6_035	MIXED017	AY769175	Poaceae	Chloridoideae (subfamily) [ <i>Eragrostis papposa</i> ; <i>Eragrostis racemosa</i> ; <i>Sporobolus ioclados</i> ]		0.69	0.24	0.00
P6_014	MIXED019	DQ655886	Poaceae	<i>Harpache schimperi</i>		0.59	0.34	0.04
P6_064	UHURU556-14	DQ655884	Poaceae	Paniceae (tribe) [ <i>Brachiaria lachnantha</i> ; <i>Panicum maximum</i> ; <i>Urochloa brachyura</i> ]		0.44	0.24	NS
P6_001	MIXED005	GU594587	Poaceae	<i>Aristida kenyensis</i>		0.15	0.44	0.01
P6_059	UHURU405-14	DQ172209	Poaceae	<i>Pennisetum</i> (genus) [ <i>Pennisetum meianum</i> ; <i>Pennisetum stramineum</i> ]		0.44	0.15	0.01
P6_083	MIXED029	EU929058	Poaceae	<i>Indigofera</i> (genus) [ <i>Indigofera circinella</i> ; <i>Indigofera hochstetteri</i> ]		0.23	0.27	NS
P6_017	MIXED044	AF274360	Fabaceae	<i>Eragrostis</i> sp. (UHURU232-14)		0.33	0.02	0.00
P6_078	UHURU232-14	DQ655884	Poaceae	Panicoideae (subfamily)		0.33	0.00	0.00
P6_037	MIXED016	EF156733	Poaceae	<i>Chloris</i> (genus) [ <i>Chloris virgata</i> ; <i>Chloris gayana</i> ]		0.21	0.10	NS
P6_086	MIXED008	EF156732	Poaceae	<i>Aristida congesta</i>		0.28	0.00	0.00
P6_106	UHURU422-14	DQ172209	Poaceae			0.23	0.02	0.02

P6_115	UHURU1233-15	EU939980	Poaceae	PACMAD clade	0.03	0.12	NS
P6_053	MATCHS38	GQ869932	Poaceae	PACMAD clade	0.08	0.02	NS
P6_048	UHURU309-14	DQ655880	Poaceae	<i>Eragrostis superba</i>	0.08	0.02	NS
P6_125	UHURU310-14	AB445386	Crassulaceae	Crassulaceae (family)	0.08	0.00	NS
P6_007	UHURU1337-15	AF274360	Fabaceae	<i>Indigofera</i> (genus)	0.08	0.00	NS
P6_118	UHURU1293-15	GQ869998	Poaceae	<i>Lintonia nutans</i>	0.03	0.05	NS
P6_043	MIXED043	KC479279	Malvaceae	<i>Grewia</i> (genus) [ <i>Grewia kakothamnos</i> ; <i>Grewia similis</i> ]	0.03	0.05	NS
P6_057	UHURU118-14	AY328142	Malvaceae	<i>Sida</i> sp. (UHURU118-14)	0.05	0.00	NS
P6_116	UHURU1233-15	GU594587	Poaceae	<i>Brachiaria deflexa</i>	0.05	0.00	NS
P6_015	MATCHS38	GQ869934	Poaceae	<i>Garnotia tenella</i>	0.03	0.02	NS
P6_107	UHURU1172-14	DQ104308	Poaceae	PACMAD clade	0.03	0.02	NS
P6_058	UHURU470-14	AM266936	Rubiaceae	<i>Pentanisia ouranogyne</i>	0.03	0.02	NS
P6_120	MIXED008	AY523507	Poaceae	Cynodonteae (tribe)	0.00	0.05	NS
P6_011	MIXED021	HQ696727	Malvaceae	Malvaceae (family) [ <i>Hibiscus calyphyllus</i> ; <i>Malva parviflora</i> ]	0.00	0.05	NS
P6_063	UHURU054-14	AF309858	Fabaceae	<i>Rhynchosia</i> (genus)	0.03	0.00	NS
P6_105	UHURU1084-14	DQ655886	Poaceae	PACMAD clade	0.03	0.00	NS
P6_034	MATCHS10	FJ847837	Phyllanthaceae	<i>Phyllanthus</i> (genus) [ <i>Phyllanthus sepialis</i> ; <i>Phyllanthus</i> sp. (UHURU699-14)]	0.03	0.00	NS
P6_026	UHURU026-14	JX870569	Fabaceae	<i>Acacia brevispica</i>	0.03	0.00	NS
P6_039	UHURU054-14	AF309858	Fabaceae	<i>Rhynchosia minima</i>	0.03	0.00	NS
P6_110	UHURU1013-14	EF688787	Amaranthaceae	<i>Psilotrichum elliotii</i>	0.03	0.00	NS
P6_044	UHURU1078-14	AY905472	Onagraceae	<i>Ludwigia stolonifera</i>	0.03	0.00	NS
P6_121	UHURU1309-15	JQ041837	Poaceae	<i>Digitaria</i> (genus)	0.00	0.02	NS
P6_111	UHURU060-14	AF460121	Asteraceae	<i>Aspilia pleuriseta</i>	0.00	0.02	NS
P6_006	UHURU1222-15	AF522975	Fabaceae	<i>Acacia mellifera</i>	0.00	0.02	NS
						Buffalo FOO	Cattle FOO
P6_024	MIXED016	EU056305	Poaceae	<i>Digitaria</i> (genus) [ <i>Digitaria milaniana</i> ; <i>Digitaria velutina</i> ; <i>Digitaria</i> spp. (UHURU429-14; UHURU1262-15)]	0.97	1.00	NS
P6_020	UHURU575-14	EF196918	Poaceae	<i>Cynodon plectostachyus</i>	0.90	0.98	NS
P6_017	MIXED044	AF274360	Fabaceae	<i>Indigofera</i> (genus) [ <i>Indigofera circinella</i> ; <i>Indigofera hochstetteri</i> ]	0.85	1.00	0.01
P6_021	UHURU978-14	DQ890472	Poaceae	<i>Pennisetum stramineum</i>	1.00	0.50	0.00
P6_025	UHURU575-14	EF196918	Poaceae	Cynodonteae (tribe)	0.46	0.96	0.00

P6_022	MIXED004	EF156683	Poaceae	Andropogonea (tribe) [ <i>Bothriochloa insculpta</i> ; <i>Cymbopogon commutatus</i> ; <i>Hyparrhenia anamesa</i> ; <i>Hyparrhenia</i> sp. aff. <i>Nubica</i> ]	0.69	0.65	NS
P6_007	UHURU1337-15	AF274360	Fabaceae	<i>Indigofera</i> (genus)	0.46	0.85	0.00
P6_008	UHURU602-14	EU939989	Poaceae	<i>Pennisetum mezianum</i>	0.56	0.69	NS
P6_001	MIXED005	GU594587	Poaceae	Paniceae (tribe) [ <i>Brachiaria lachnantha</i> ; <i>Panicum maximum</i> ; <i>Urochloa brachyura</i> ]	0.87	0.31	0.00
P6_042	UHURU602-14	AY769175	Poaceae	PACMAD clade	0.36	0.75	0.00
P6_035	MIXED017	AY769175	Poaceae	PACMAD clade [ <i>Dinebra retroflexa</i> ; <i>Enteropogon macrostachyus</i> ; <i>Melinis repens</i> ; <i>Microchloa kunthii</i> ]	0.38	0.65	0.02
P6_037	MIXED016	EF156733	Poaceae	Panicoideae (subfamily)	0.92	0.08	0.00
P6_058	UHURU470-14	AM266936	Rubiaceae	<i>Pentanisia ouranogyne</i>	0.36	0.58	NS
P6_011	MIXED021	HQ696727	Malvaceae	Malvaceae (family) [ <i>Hibiscus calyphyllus</i> ; <i>Malva parviflora</i> ]	0.62	0.29	0.01
P6_026	UHURU026-14	JX870569	Fabaceae	<i>Acacia brevispica</i>	0.59	0.23	0.00
P6_033	UHURU890-14	EF156683	Poaceae	<i>Themeda triandra</i>	0.62	0.19	0.00
P6_034	MATCHS10	FJ847837	Phyllanthaceae	<i>Phyllanthus</i> (genus) [ <i>Phyllanthus sepialis</i> ; <i>Phyllanthus</i> sp. (UHURU699-14)]	0.31	0.38	NS
P6_023	UHURU596-14	AY328160	Malvaceae	<i>Melhania ovata</i>	0.49	0.13	0.00
P6_019	UHURU014-14	AY328160	Malvaceae	<i>Abutilon mauritianum</i>	0.49	0.08	0.00
P6_040	MIXED036	AY216061	Asteraceae	Asteraceae (family) [ <i>Vernonia galamensis</i> ; <i>Gutenbergia boranensis</i> ; <i>Gutenbergia cordifolia</i> ; <i>Kleinia squarrosa</i> ; <i>Solanecio angulatus</i> ; <i>Solanecio cydoniifolius</i> ; Asteraceae sp. (UHURU417-14); <i>Vernonia</i> sp. (UHURU129-14)]	0.05	0.44	0.00
P6_064	UHURU556-14	DQ655884	Poaceae	<i>Harpachne schimperi</i>	0.00	0.48	0.00
P6_051	MATCHS38	AY116259	Poaceae	PACMAD clade [ <i>Brachiaria eruciformis</i> ; <i>Setaria sphacelata</i> ; <i>Setaria verticillata</i> ; <i>Sporobolus africanus</i> ; <i>Sporobolus festivus</i> ; <i>Sporobolus pyramidalis</i> ; <i>Sporobolus stapfianus</i> ; <i>Chrysopogon plumosus</i> ; <i>Setaria</i> sp. (UHURU639-14); <i>Sporobolus</i> sp. (UHURU593-14)]	0.36	0.12	0.01
P6_049	UHURU1242-15	AY116262	Poaceae	PACMAD clade [Poaceae sp. (UHURU1242-15)]	0.28	0.19	NS
P6_041	MATCHS38	GQ869932	Poaceae	<i>Garnotia</i> (genus)	0.44	0.00	0.00
P6_038	MIXED043	KC479279	Malvaceae	<i>Grewia</i> sp.	0.31	0.08	0.01
P6_053	MATCHS38	GQ869932	Poaceae	PACMAD clade	0.26	0.08	0.05
P6_014	MIXED019	DQ655886	Poaceae	Chloridoideae (subfamily) [ <i>Eragrostis papposa</i> ; <i>Eragrostis racemosa</i> ; <i>Sporobolus ioclados</i> ]	0.00	0.31	0.00
P6_057	UHURU118-14	AY328142	Malvaceae	<i>Sida</i> sp. (UHURU118-14)	0.10	0.17	NS
P6_015	MATCHS38	GQ869934	Poaceae	<i>Garnotia tenella</i>	0.23	0.04	0.01
P6_027	UHURU596-14	AY328160	Malvaceae	<i>Melhania</i> (genus)	0.26	0.00	0.00
P6_066	UHURU174-14	EU497701	Euphorbiaceae	<i>Croton dichogamous</i>	0.21	0.04	0.04
P6_048	UHURU309-14	DQ655880	Poaceae	<i>Eragrostis superba</i>	0.13	0.12	NS
P6_043	MIXED043	KC479279	Malvaceae	<i>Grewia</i> (genus) [ <i>Grewia kakothamnos</i> ; <i>Grewia similis</i> ]	0.21	0.04	0.04

P6_036	UHURU470-14	AM266936	Rubiaceae	<i>Pentanisia</i> (genus)		0.00	0.23	0.00
P6_003	MIXED001	FJ009898	Fabaceae	<i>Acacia</i> (genus) [ <i>Acacia drepanolobium</i> ; <i>Acacia ethiaca</i> ; <i>Acacia gerrardii</i> ; <i>Acacia tortilis</i> ]		0.15	0.08	NS
P6_078	UHURU232-14	DQ655884	Poaceae	<i>Eragrostis</i> sp. (UHURU232-14)		0.00	0.23	0.00
P6_098	UHURU1115-14	AY794776	Euphorbiaceae	<i>Acalypha californica</i>		0.15	0.06	NS
P6_084	MATCHS38	GQ869932	Poaceae	PACMAD clade		0.21	0.00	0.00
P6_039	UHURU054-14	AF309858	Fabaceae	<i>Rhynchosia minima</i>		0.13	0.04	NS
P6_010	UHURU815-14	HM488394	Malvaceae	<i>Hermannia uhligii</i>		0.10	0.06	NS
P6_012	MIXED022	AY328160	Malvaceae	<i>Hibiscus</i> (genus) [ <i>Hibiscus micranthus</i> ; <i>Hibiscus meyeri</i> ]		0.13	0.02	NS
P6_087	MIXED033	AB162025	Acanthaceae	<i>Ruellia</i> (genus) [ <i>Ruellia patula</i> ; <i>Ruellia prostrata</i> ]		0.00	0.13	0.02
P6_016	UHURU605-14	JN249677	Euphorbiaceae	<i>Euphorbia inaequilatera</i>		0.00	0.13	0.04
P6_009	UHURU1217-15	AY792527	Poaceae	<i>Leersia hexandra</i>		0.13	0.00	0.02
P6_083	MIXED029	EU929058	Poaceae	<i>Pennisetum</i> (genus) [ <i>Pennisetum mezianum</i> ; <i>Pennisetum stramineum</i> ]		0.13	0.00	0.02
P6_030	UHURU030-14	EF688731	Amaranthaceae	<i>Achyranthes aspera</i>		0.13	0.00	0.04
P6_089	UHURU1309-15	AF127058	Poaceae	<i>Echinochloa pyramidalis</i>		0.13	0.00	0.03
P6_063	UHURU054-14	AF309858	Fabaceae	<i>Rhynchosia</i> (genus)		0.08	0.04	NS
P6_065	UHURU407-14	DQ924225	Ebenaceae	<i>Euclea divinorum</i>		0.08	0.04	NS
P6_086	MIXED008	EF156732	Poaceae	<i>Chloris</i> (genus) [ <i>Chloris virgata</i> ; <i>Chloris gayana</i> ]		0.00	0.12	0.05
P6_032	UHURU439-14	AF141712	Asteraceae	<i>Helichrysum glumaceum</i>		0.00	0.12	NS
P6_093	MATCHS38	GQ869932	Poaceae	PACMAD clade		0.10	0.00	NS
P6_108	UHURU030-14	EF688731	Amaranthaceae	<i>Achyranthes</i> (genus)		0.10	0.00	NS
P6_096	UHURU030-14	EF688734	Amaranthaceae	<i>Achyranthes</i> (genus)		0.10	0.00	0.04
P6_018	UHURU1078-14	AY594496	Anacardiaceae	Anacardiaceae (family)		0.08	0.02	NS
P6_077	UHURU1288-15	AJ558038	Aizoaceae	<i>Zaleya pentandra</i>		0.00	0.10	NS
P6_080	UHURU1108-14	GU246085	Burseraceae	Burseraceae (family)		0.08	0.00	NS
P6_045	MATCHS38	GQ869932	Poaceae	<i>Garnotia acutigluma</i>		0.08	0.00	NS
P6_059	UHURU405-14	DQ172209	Poaceae	<i>Aristida kenyensis</i>		0.03	0.04	NS
P6_054	UHURU852-14	AY122435	Capparaceae	<i>Boscia angustifolia</i>		0.00	0.06	NS
P6_060	UHURU1352-15	AF274367	Fabaceae	<i>Indigofera</i> (genus)		0.05	0.00	NS
P6_110	UHURU1013-14	EF688787	Amaranthaceae	<i>Psilotrichum elliotii</i>		0.05	0.00	NS
P6_061	UHURU1108-14	FJ466473	Burseraceae	<i>Commiphora habessinica</i>		0.05	0.00	NS

P6_118	UHURU1293-15	GQ869998	Poaceae	<i>Lintonia nutans</i>	0.05	0.00	NS
P6_105	UHURU1084-14	DQ655886	Poaceae	PACMAD clade	0.03	0.02	NS
P6_044	UHURU1078-14	AY905472	Onagraceae	<i>Ludwigia stolonifera</i>	0.03	0.02	NS
P6_046	UHURU1115-14	JN207679	Euphorbiaceae	<i>Euphorbia</i> (genus)	0.03	0.00	NS
P6_099	UHURU299-14	HE577609	Amaranthaceae	<i>Chenopodium</i> (genus)	0.03	0.00	NS
P6_111	UHURU060-14	AF460121	Asteraceae	<i>Aspilia pleuriseta</i>	0.03	0.00	NS
P6_122	UHURU1204-15	AJ225792	Rhamnaceae	<i>Scutia myrtina</i>	0.03	0.00	NS
P6_006	UHURU1222-15	AF522975	Fabaceae	<i>Acacia mellifera</i>	0.03	0.00	NS
P6_067	UHURU1312-15	AJ875117	Rutaceae	<i>Teclea nobilis</i>	0.03	0.00	NS
P6_114	UHURU1233-15	EU939980	Poaceae	PACMAD clade	0.00	0.02	NS
P6_028	UHURU721-14	HE795473	Geraniaceae	<i>Monsonia angustifolia</i>	0.00	0.02	NS
P6_116	UHURU1233-15	GU594587	Poaceae	<i>Brachiaria deflexa</i>	0.00	0.02	NS
P6_095	UHURU1352-15	AF274367	Fabaceae	<i>Indigofera</i> sp. (UHURU1352-15)	0.00	0.02	NS

**Table S7.** Identification of dietary sequences based on family-specific ITS markers. The relative frequency of occurrence (FOO) of each sequence is reported as a proportion of subset of samples that yielded sequences from each respective marker (Table S2). The sequence identifier prefix indicates the relevant plant family and marker (Poa = Poaceae; Ast = Asteraceae; Cyp = Cyperaceae). Sequence information for each ITS metabarcode sequence includes the best match (% identity expressed as a proportion) to a reference sequence in the local Mpala or EMBL database (including references to BOLD Process IDs in the archived local reference library and EMBL accession numbers, respectively). When exact matches were made to multiple taxa, assignments were adjusted to the next-highest taxonomic level (shown in parentheses) and each matching species is listed in brackets. Representative BOLD Process ID numbers are given in parentheses for exact matches to morphospecies that have not been identified to species-level. When no exact match was made to either database, the finest taxonomic level including all best-matching taxa is given in parentheses.

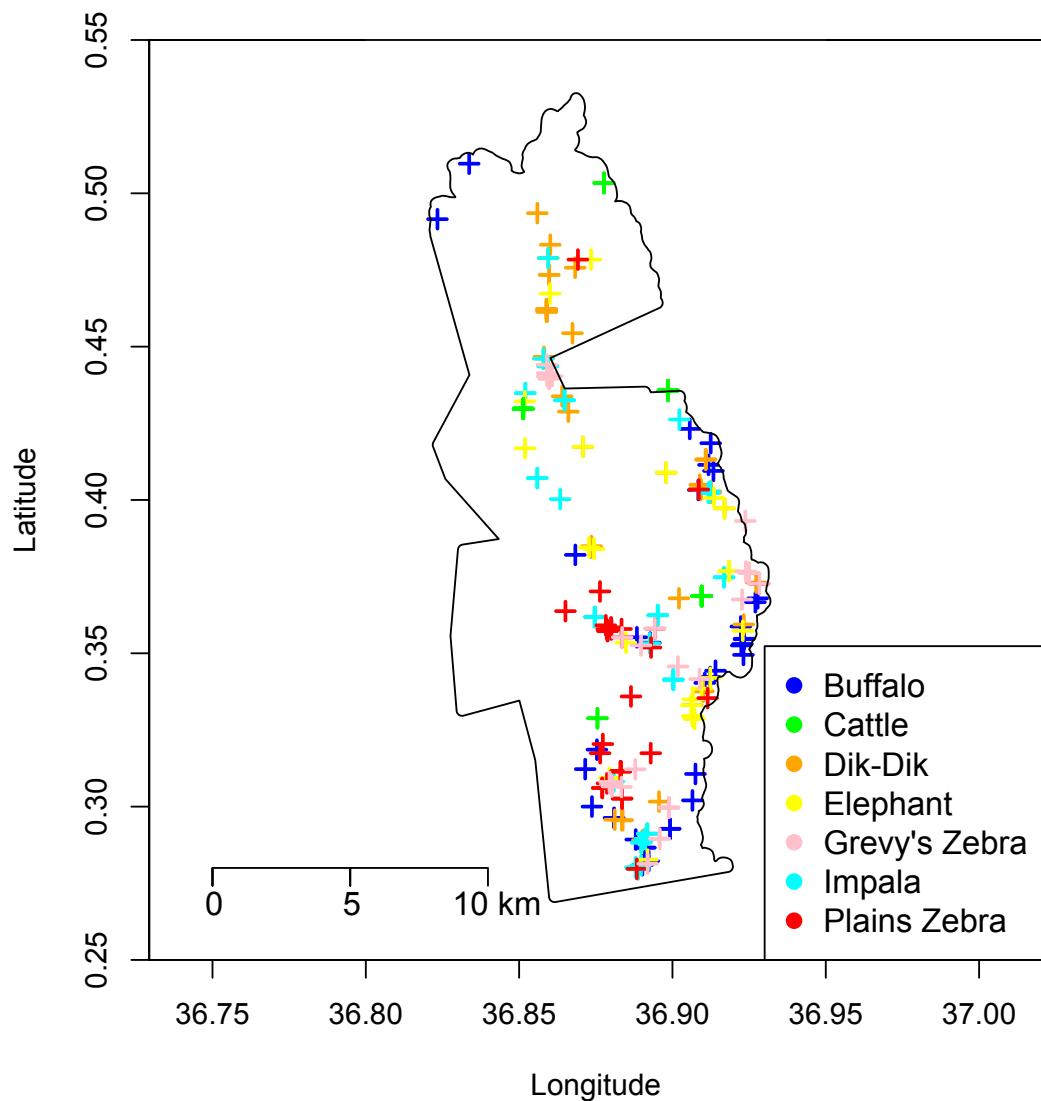
Sequence Information						Frequency of Occurrence							
Seq.	Local	Local	EMBL	EMBL	Best Identity	Buffalo	Cattle	Dik-Dik	Elephant	Grevy's	Impala	Plains	Total
ITSast_010	0.82	UHURU581-14	1.00	EU527241	<i>Hirpicium diffusum</i> <i>Gutenbergia</i> (genus)	1.00	1.00	0.44	0.95	1.00	0.98	0.00	0.81
ITSast_004	1.00	Ast_MIXED03	0.76	EF155793	[ <i>Gutenbergia boranensis</i> ; <i>Gutenbergia cordifolia</i> ]	1.00	0.86	0.87	0.55	1.00	0.76	0.00	0.77
ITSast_005	1.00	UHURU457-14	0.95	AY953930	<i>Emilia discifolia</i>	1.00	0.14	0.54	0.65	1.00	0.73	1.00	0.55
ITSast_007	1.00	UHURU581-14	0.96	FJ861498	<i>Osteospermum vaillantii</i>	0.00	0.14	0.38	0.65	1.00	0.38	0.00	0.36
ITSast_011	1.00	UHURU673-14	0.97	AY445223	<i>Helichrysum glumaceum</i>	0.00	0.55	0.18	0.15	0.00	0.36	0.00	0.31
ITSast_020	1.00	UHURU418-14	0.99	AF374885	Asteraceae sp. (UHURU418-14)	0.00	0.03	0.08	0.25	0.00	0.07	0.00	0.09
ITSast_022	1.00	UHURU091-14	0.98	GU818570	<i>Kleinia squarrosa</i>	0.00	0.00	0.05	0.10	0.00	0.00	0.00	0.03
ITSast_049	1.00	UHURU1143-14	0.98	GU818711	<i>Solanecio angulatus</i>	0.00	0.00	0.03	0.10	0.00	0.00	0.00	0.02
ITSast_040	1.00	UHURU1199-15	0.98	AB435132	<i>Helichrysum</i> sp. (UHURU1199-15)	0.00	0.00	0.03	0.05	0.00	0.00	0.00	0.01
ITSast_002	1.00	Ast_MIXED02	0.99	AB435132	Asteraceae (family) [ <i>Psiadia punctulata</i> , <i>Conyzia stricta</i> , Asteraceae sp. (UHURU396-14)]	0.00	0.00	0.03	0.00	0.00	0.02	0.00	0.01
ITSast_050	1.00	UHURU268-14	0.99	AY458004	<i>Sonchus</i> sp. (UHURU268-14)	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.01
ITSast_053	1.00	UHURU058-14	0.94	AY303437	<i>Aspilia pleuriseta</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.01
ITSast_009	0.90	UHURU1143-14	1.00	KC311155	<i>Senecio hadiensis</i>	0.00	0.00	0.03	0.00	0.00	0.00	0.00	0.01
ITSpoa_004	1.00	Poa_MIXED07	0.97	U46649	<i>Pennisetum</i> (genus) [ <i>Pennisetum meyanum</i> ; <i>Pennisetum stramineum</i> ]*	1.00	1.00	0.94	1.00	1.00	0.98	0.98	0.98
ITSpoa_001	1.00	UHURU1262-15	0.97	AF019826	<i>Digitaria</i> sp. (UHURU1262-15)	0.97	1.00	0.98	0.81	0.90	1.00	0.80	0.94
ITSpoa_003	1.00	UHURU603-14	0.92	AF019832	<i>Pennisetum meyanum</i> *	0.79	0.77	0.15	0.67	0.97	0.21	0.98	0.63
ITSpoa_015	1.00	UHURU677-14	0.93	HM347028	<i>Panicum maximum</i>	0.92	0.60	0.49	0.96	0.38	0.23	0.02	0.49
ITSpoa_002	1.00	UHURU888-14	0.95	FJ766165	<i>Themeda triandra</i>	0.85	0.63	0.11	0.07	0.46	0.23	0.95	0.48

ITSpoa_034	1.00	UHURU1170-14	1.00	AM900998	<i>Eragrostis papposa</i> *	0.05	0.67	0.15	0.00	0.92	0.67	0.39	0.44
ITSpoa_005	0.89	UHURU677-14	1.00	AY346357	<i>Brachiaria platynota</i>	0.05	0.48	0.51	0.37	0.05	0.42	0.02	0.29
ITSpoa_013	1.00	UHURU1233-15	0.99	HM347014	<i>Brachiaria deflexa</i> *	0.15	0.46	0.13	0.33	0.33	0.35	0.20	0.28
ITSpoa_053	1.00	UHURU915-14	1.00	DQ005028	<i>Bothriochloa insculpta</i>	0.23	0.38	0.02	0.00	0.18	0.21	0.88	0.28
ITSpoa_027	1.00	UHURU558-14	0.97	GU359113	<i>Harpachne schimperi</i>	0.08	0.42	0.13	0.00	0.51	0.31	0.27	0.26
ITSpoa_019	1.00	UHURU1345-15	0.99	FJ626356	<i>Setaria verticillata</i>	0.23	0.29	0.11	0.41	0.05	0.38	0.02	0.21
ITSpoa_077	1.00	UHURU235-14	0.95	AF498394	<i>Eragrostis</i> sp. (UHURU235-14)	0.05	0.58	0.00	0.07	0.54	0.00	0.02	0.19
ITSpoa_035	1.00	Poa_MIXED01	0.99	HM347010	<i>Digitaria</i> (genus) [ <i>Digitaria milaniana</i> ; <i>Digitaria velutina</i> ]	0.00	0.10	0.30	0.11	0.05	0.48	0.02	0.16
ITSpoa_025	1.00	UHURU1174-14	0.99	GU359224	<i>Tragus berteronianus</i>	0.00	0.19	0.17	0.00	0.15	0.33	0.07	0.15
ITSpoa_026	1.00	UHURU309-14	1.00	DQ655825	<i>Eragrostis superba</i>	0.18	0.23	0.02	0.04	0.21	0.10	0.07	0.13
ITSpoa_073	0.92	UHURU902-14	1.00	GU359303	<i>Eragrostis tenuifolia</i>	0.03	0.06	0.02	0.00	0.38	0.13	0.24	0.12
ITSpoa_011	1.00	UHURU1257-15	0.92	AY129708	<i>Brachiaria deflexa</i> *	0.05	0.21	0.06	0.15	0.10	0.21	0.00	0.12
ITSpoa_058	1.00	UHURU792-14	0.92	AY129695	<i>Setaria sphacelata</i> *	0.08	0.04	0.00	0.00	0.03	0.00	0.66	0.11
ITSpoa_018	1.00	UHURU1279-15	0.97	AF498394	<i>Eragrostis papposa</i> *	0.00	0.40	0.17	0.00	0.05	0.00	0.02	0.11
ITSpoa_029	1.00	UHURU1029-14	0.93	AY129708	<i>Urochloa brachyura</i>	0.03	0.00	0.13	0.19	0.03	0.27	0.00	0.09
ITSpoa_055	1.00	UHURU791-14	0.91	AY129695	<i>Setaria sphacelata</i> *	0.03	0.00	0.00	0.00	0.00	0.00	0.59	0.09
ITSpoa_079	1.00	UHURU1163-14	1.00	AY746595	<i>Melinis repens</i>	0.08	0.13	0.02	0.11	0.18	0.06	0.02	0.09
ITSpoa_178	0.94	UHURU1170-14	1.00	AM900996	<i>Eragrostis papposa</i> *	0.03	0.02	0.04	0.04	0.10	0.23	0.05	0.08
ITSpoa_068	1.00	UHURU1221-15	0.99	AY346345	<i>Brachiaria lachnantha</i> *	0.08	0.02	0.00	0.00	0.05	0.00	0.34	0.07
ITSpoa_141	0.95	UHURU1295-15	1.00	AF019832	<i>Cenchrus ciliaris</i>	0.03	0.17	0.00	0.07	0.18	0.00	0.02	0.07
ITSpoa_040	0.86	Poa_MIXED07	1.00	AY129705	<i>Panicum deustum</i>	0.36	0.02	0.00	0.00	0.00	0.00	0.00	0.05
ITSpoa_074	1.00	UHURU1076-14	0.91	AB353352	<i>Echinochloa pyramidalis</i> *	0.26	0.00	0.02	0.07	0.00	0.00	0.00	0.04
ITSpoa_051	0.96	UHURU893-14	1.00	DQ171970	<i>Aristida adscensionis</i>	0.00	0.00	0.06	0.00	0.15	0.00	0.00	0.03
ITSpoa_085	1.00	Poa_MIXED06	0.87	EU646091	<i>Sporobolus</i> (genus) [ <i>Sporobolus staphianus</i> ; <i>Sporobolus festivus</i> ]	0.00	0.02	0.04	0.00	0.03	0.02	0.05	0.02
ITSpoa_044	1.00	UHURU1333-15	0.96	KF163627	<i>Echinochloa pyramidalis</i> *	0.03	0.00	0.00	0.19	0.00	0.00	0.00	0.02
ITSpoa_012	1.00	UHURU1295-15	1.00	AY346359	<i>Brachiaria eruciformis</i>	0.03	0.00	0.00	0.00	0.00	0.00	0.10	0.02
ITSpoa_124	0.99	UHURU1135-14	1.00	AF190752	<i>Cymbopogon caesius</i>	0.08	0.02	0.00	0.00	0.00	0.00	0.02	0.02
ITSpoa_076	1.00	UHURU1375-15	0.99	EF153061	<i>Dinebra retroflexa</i> *	0.00	0.06	0.00	0.00	0.00	0.00	0.00	0.01
ITSpoa_043	1.00	UHURU871-14	0.86	EF153034	<i>Sporobolus agrostoides</i>	0.03	0.00	0.00	0.04	0.00	0.00	0.00	0.01
ITSpoa_036	1.00	UHURU1327-15	0.97	EF153061	<i>Dinebra retroflexa</i> *	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.01

ITSpoa_020	1.00	UHURU1094-14	0.96	EU528606	<i>Pennisetum hohenackeri</i>	0.03	0.00	0.00	0.04	0.00	0.00	0.00	0.01
ITSpoa_228	1.00	UHURU595-14	0.85	AY129721	<i>Sporobolus</i> sp. (UHURU595-14)	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00
ITSpoa_258	1.00	UHURU1353-15	0.91	GU359303	<i>Sporobolus ioclados</i>	0.00	0.00	0.00	0.00	0.00	0.02	0.00	0.00
ITSpoa_266	1.00	UHURU1373-15	1.00	DQ655840	<i>Enneapogon cenchroides</i>	0.00	0.00	0.00	0.04	0.00	0.00	0.00	0.00
ITSpoa_237	0.99	UHURU1221-15	1.00	AY346345	<i>Brachiaria lachnantha*</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
ITSpoa_082	0.91	UHURU1290-15	1.00	AF190759	<i>Heteropogon contortus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.00
ITScyp_007	0.64	UHURU1041-14	0.96	AB206265	<i>Schoenoplectiella</i> sp.	1.00	0.00	0.00	0.80	1.00	1.00	0.00	0.89
ITScyp_058	0.88	UHURU167-14	0.97	JX644854	<i>Cyperus</i> sp.	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.11

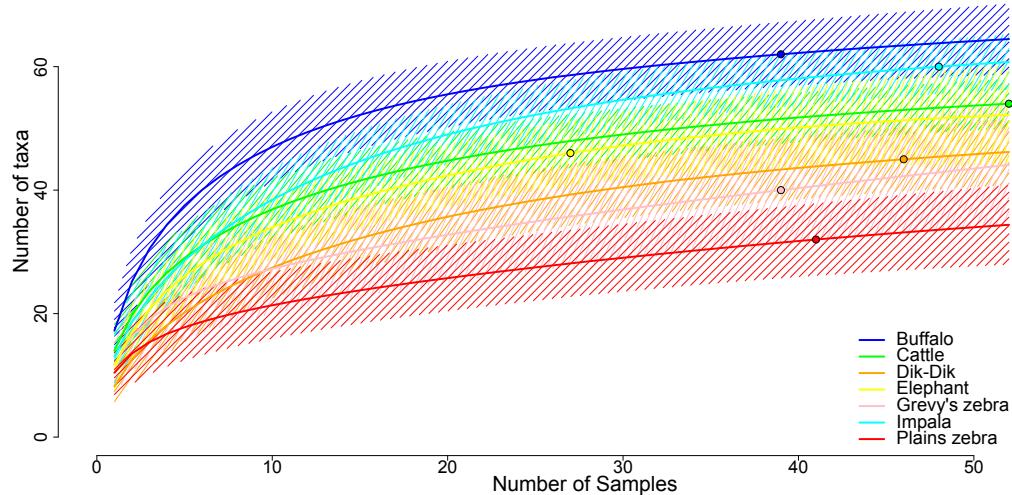
\*Possible intraspecific variation in ITS sequences.

**Figure S1.** Map of sample collection locations across Mpala Research Centre, Laikipia, Kenya.

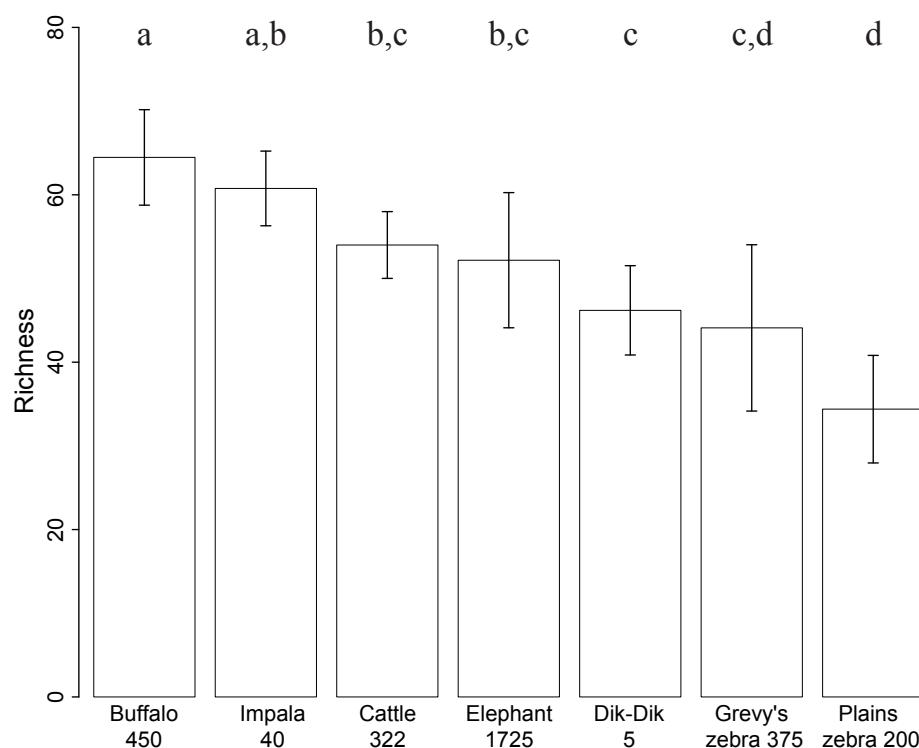


**Figure S2.** Comparisons of dietary richness (i.e., niche breadth), among LMH species. (A) Species-accumulation curves based on rarefaction and extrapolation of unique *trnL*-P6 sequences ( $\pm 95\%$  CI) approach an asymptote for each LMH species (points on each curve indicate the *observed* richness and sample size for that species). (B) Comparisons of richness at the maximum sample size ( $N = 52$ ) show that buffalo diets were richer than most (95% CI overlaps only with impala) and plains zebra diets were poorer than most (95% CI overlaps only with Grevy's zebra and dik-dik). The body mass (kg) of each LMH species appears along the X-axis; dietary richness did not monotonically vary with log-transformed body mass ( $F_{1,5} = 0.06$ ,  $R^2 = 0.01$ ,  $P > 0.8$ ).

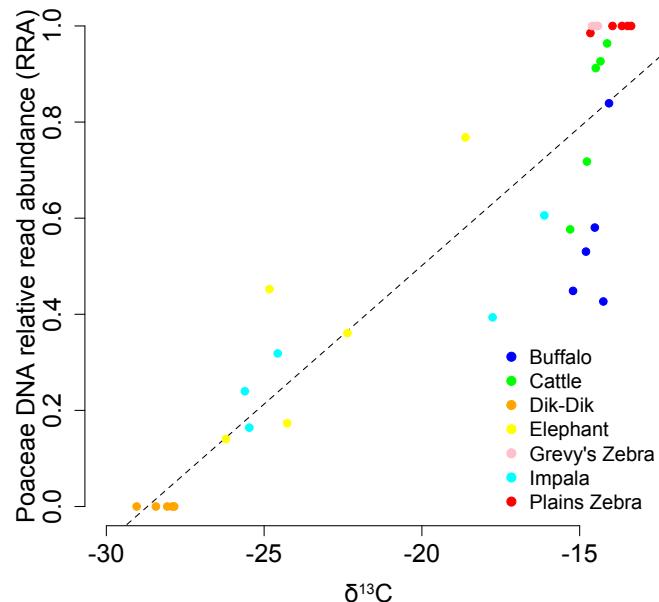
A



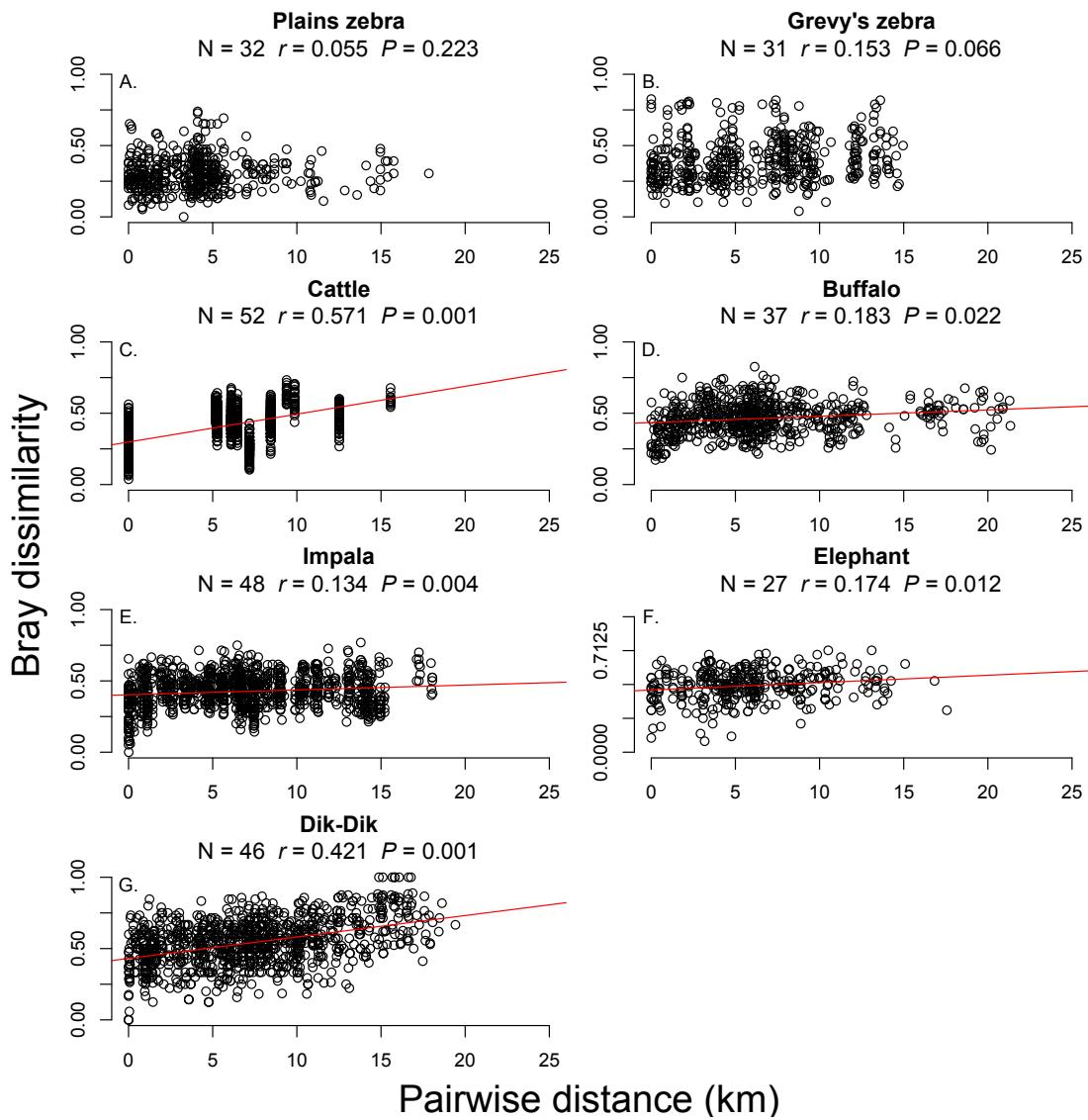
B



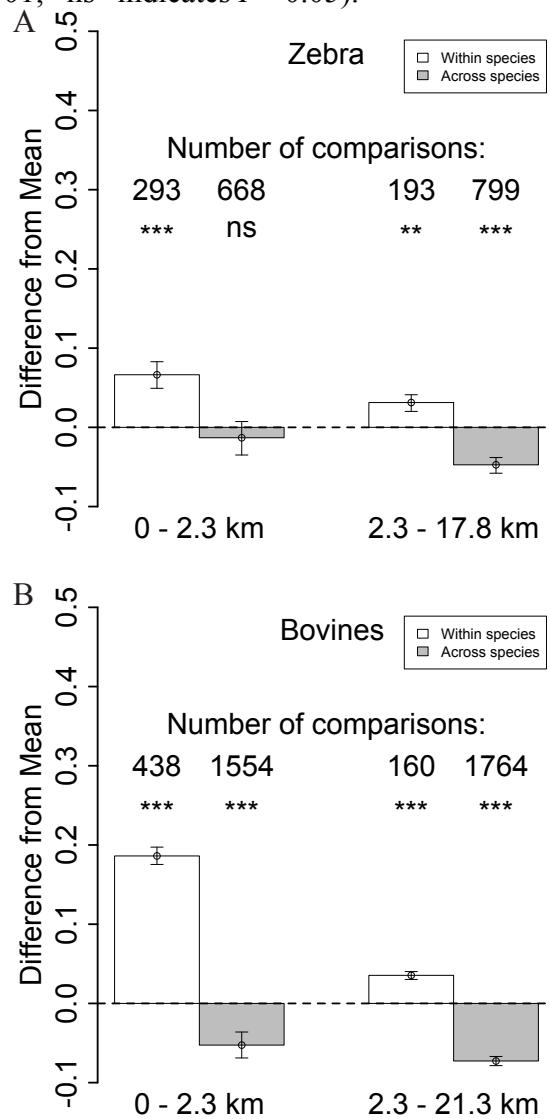
**Figure S3.** Correlation between DNA metabarcode RRA of grasses (Y axes) and carbon stable isotope values (X axes). The correlation between grass RRA and the measured  $\delta^{13}\text{C}$  values in the subset of samples selected for stable isotope analysis was significant ( $F_{1,31} = 128.1$ ,  $R^2 = 0.81$ ,  $P < 0.01$ ). These data correspond to main text Fig. 2E, but show  $\delta^{13}\text{C}$  and RRA of each sample instead of the modeled population-level C<sub>4</sub> consumption and mean RRA.



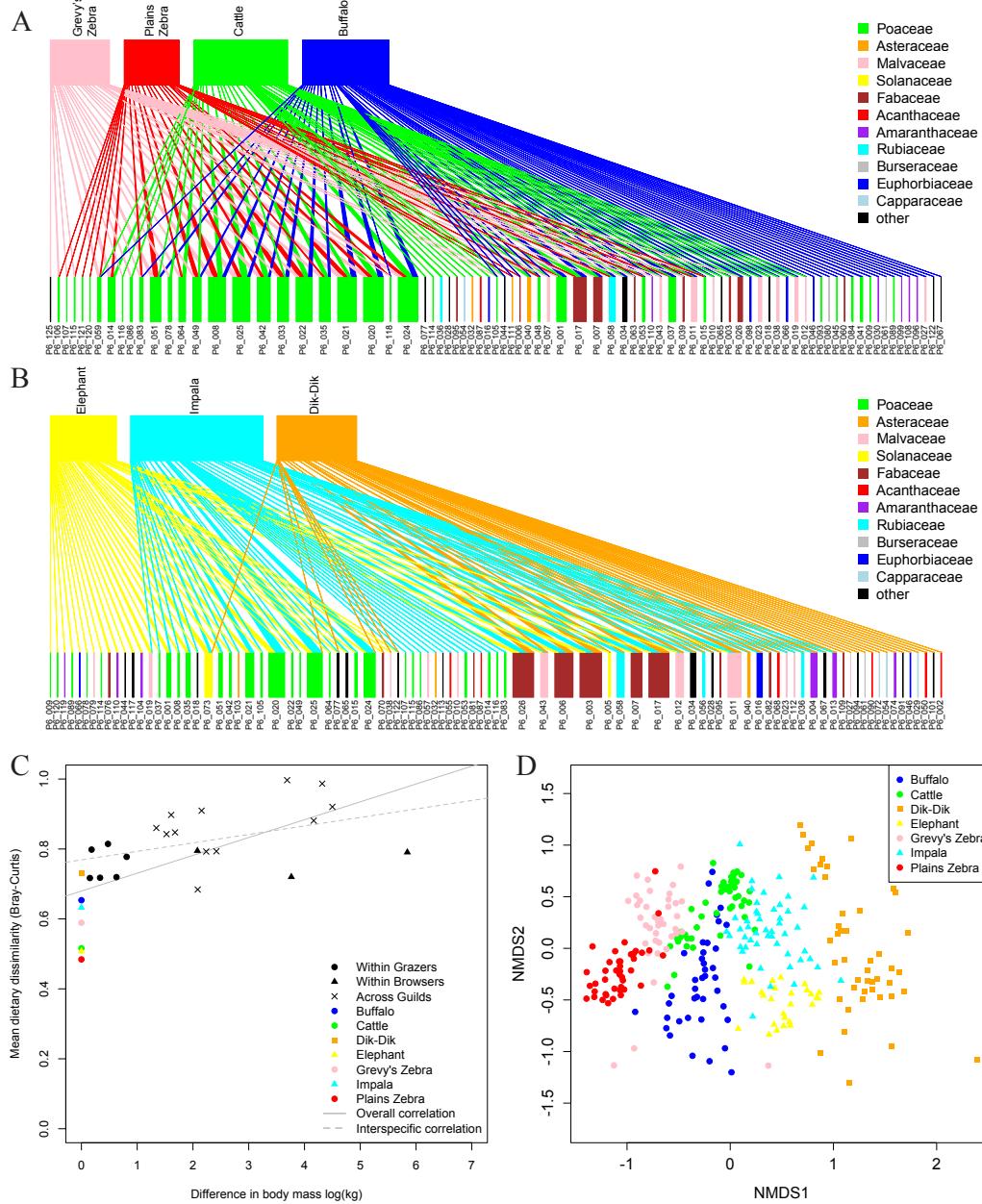
**Figure S4.** Correlations between dietary dissimilarity and geographic distance (km) between sample locations. Cattle samples have a more spatially discrete distribution because they were collected from different individuals within herds sharing a corral.



**Figure S5.** Tests for pairwise similarity of intra- and interspecific samples collected close (0 – 2.3 km) and far (>2.3 km) from each other for (A) zebra and (B) bovine species. Comparisons were standardized by the mean dietary dissimilarity of all samples in each focal pair (i.e., the null expectation = 0), such that positive values indicate comparisons that are more similar than expected and negative values indicate comparisons that are less similar than expected ( $\pm 95\%$  CI based on 1000 bootstrap samples). The number of samples included in each comparison is listed above the bars, along with asterisks indicating the results of permutation tests (\* $P \leq 0.05$ ; \*\* $P \leq 0.01$ ; \*\*\* $P \leq 0.001$ ; “ns” indicates  $P > 0.05$ ).



**Figure S6.** Results of RRA-based analyses of *trnL*-P6. Bipartite networks show sequences occurring in the diets of (A) grazers and (B) non-grazers, as in Fig. 1 of the main text, but with the sizes of the lower boxes scaled to reflect their mean RRA in samples from each LMH species. Sequence identifiers are beneath lower boxes (Table S3). (C) Correlations between mean pairwise dietary dissimilarities. As in Fig. 3 of the main text, intraspecific comparisons are indicated by colors (body-mass difference = 0), while interspecific comparisons are distinguished by shapes (body mass difference > 0); lines show regressions fit for all comparisons (solid line:  $F_{1,26} = 18.19$ ,  $R^2 = 0.41$ ,  $P < 0.001$ ) and for interspecific comparisons only (dashed line:  $F_{1,19} = 4.75$ ,  $R^2 = 0.20$ ,  $P < 0.05$ ). (D) Dietary dissimilarity among species visualized using NMDS.



**Figure S7.** Results of analyses of family-specific Poaceae (A-B) and Asteraceae (C-D) ITS markers. Bipartite networks (A,C) show plant species detected in LMH diets. Sequence identifiers are beneath the lower boxes (Table S7). Dietary niche overlap is visualized using NMDS (B,D).

